us-09-938-703-6.rai

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Page 5

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                                                                                                                                                                                                                          61 LKSMTDIYLLNIAISDLFFILTVPFWAHYAAAQWDFGNTWCQLLTGLYFIGFFSGIFFII 120
                                                                                                                                                                     1 MDZQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
                                      Gaps
                                      0;
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APPLICANT: LI, YI
APPLICANT: DE INVENTION: CHEMOKINE RECEPTOR HIGHRIO (AS AMENDED)
TITLE OF INVENTION: CHEMOKINE RECEPTOR HIGHRIO (AS AMENDED)
84.8%; Score 952; DB 4; Length 352; 98.9%; Pred. No. 3.9e-85; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES.
STREES: 4DDRESSEE: SERNE, FESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36,688
RRR: 1488.1150000/EKS/KLM
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119 IILLIIDRXLAVVHAVFALKARTVTFGVVTSVIIWVVAVFASLPGIIFTRSQKEGLHYTC 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDYQVSSP--IYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILLLINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN CHEMOKINE RECEPTOR HDGNR10 (AS AMENDED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/08466343D
Patent No. 6025154
CENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CERMONING HOGHEN G-PROTE
CORRESPONDENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: STRNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 776; DB 4; Length 35. Pred, No. 5.3e-68; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
OPERARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,343D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REGISTRATION NUMBER: 1488.1150000/EKS/KIM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 79.0%; Pred. No. 5.3e
Matches 147; Conservative 17; Mismatches
            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,984A
FILING DATE: OCTOBER 3, 1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                            ATG50023
                                                                                                                                                                                                      34,344
                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPRONE: 610 270 5024
TELEFAX: 610 270 5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.2%;
79.0%;
SOFTWARE: MICROSOFT WORD
                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                       NAME: William T. Han
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                    TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | |||:
181 SPHFPH 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 20005
                                                                                                                                               FILING DATE:
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US-08-466-343D-9
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APPLICANT: Kwon, Douglas S.
APPLICANT: Won Knooyk, Yuette
APPLICANT: van Knooyk, Yuette
APPLICANT: Geijtenbeck, Theo
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
TITLE OF INVENTION: CELLS
FILLE REFERENCE: 1049-1-017
CURRENT APPLICATION NUMBER: US/09/517,605
CURRENT FILING DATE: 2000-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 LITIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MOYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
                         121 LLITIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Derk Bergsma, Mary Brawner, and Usman Shabon TITLE OF INVENTION: NO. 6348055el Mouse Genomic Clone of the CCTITLE OF INVENTION: CKR5 Receptor NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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Pred. No. 1.4e-83;
3; Mismatches 2; Indels
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MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithAilne Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08724984A ; Patent No. 6388055 GENERAL INFORMATION:
                                                                                                                                                                                                                                                 Sequence 5, Application US/09517605
Patent No. 6391567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.4%;
97.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 97.3
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-517-605-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HFPY 184
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181 HEPY 184
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US-08-724-984A-2
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Human monocyte che
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Non-endogenous hum
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Inactive human CCR
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Inactive human CCR
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                                                                                                                                                                                                           CCR5 protein
HIV-1 co-rec
                                                                                                                                                                                                                                                  CCR5 protein
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                                                                                                   Human CC chemokine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human CC chemokine receptor 5 (CCR5) A127V variant.
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SUMMARIES
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                                                                                                                           08-JUN-1998 (first entry)
                                                             8
                                                             Length
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Domain
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                                                                                                                                                                                                                                                                                              Result
                                                                  No
No
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-MODEL-frame+_Li2p.model_DEV=xlp
-G-/cgn2_1/USPPO_spool/USO9938703/runat_03062003_161406_22796/app_query.fasta_1.1870
-G-/cgn2_1/USPPO_spool/USO9938703/runat_03062003_161406_22796/app_query.fasta_1.1870
-DB-A_Geneseq_101002_-OPMT-fastan_SOFFIX*-rag_-MINMATCH-0.1 -LOOPCI-0
-LIST-AS_-DOCALIGN-200 -TRANS-INMAT-0.0 -TRANS-INMAN-0.0
-USFX--0 -UNITS-bits -START-1 -END--1 -MATRIX-blosum62_-TRANS-INMAN-0.0
-GCALIGN-200 -TRE_COCALIGN-200 -TRANS-INMAN-0.0
-GCALIGN-200 -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXIEN-200000000
-USFR-USO9938703_GCGN_1 _1.62_@runat_03062003_161406_22796_-NCPU-6
-ICPU-3
-NO_MARP -LARGOGDRY -NORM-SOFFICE-0 -MAIR_-DSPBLOCK-100 -LONGIGG
-DSY_TIMEOUT=120 -WARR TIMEOUT=30 -TREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDOP=6 -DELEXT=7
                                                                                                                                                                       (without alignments)
5149.005 Million cell updates/sec
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                                                                                                                                                                                                                                                                             GAATTCCCCCAACAGAGCCA......AGTAGATTAGATCCGAATTC 1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Sins2/goddta/geneseq/geneseqp-embl/AA1980.DAT:*
| Sins2/goddta/geneseq/geneseqp-embl/AA1981.DAT:*
| Sins2/goddta/geneseq/geneseqp-embl/AA1981.DAT:*
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                                                                                                                                               June 3, 2003, 18:39:24; Search time 74.6348 Seconds
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/SIDS2/gcgdata/geneseq/genesegp-embl/AA1990.DAT:
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/SIDS2/gcgdata/geneseq/genesegp-embl/AA1993.DAT:
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/SIDS2/gcgdata/geneseg/genesegp-embl/AA1998.
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                                              Compugen Ltd.
                                                                                                         - protein search, using frame_plus_n2p model
                        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                           Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq length: 0
seq length: 200000000
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Database :

Minimum DB

Searched:

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1095 CTATGCCTTTGTCGGGGAGAAGTTCAGAAACTACCTCTTAGTCTTCTTCCAAAAGCACAT 1154
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                                                                                                                                                                                                                                                                                                                                                                                                                 795 AAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTCGGG
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                                                                                                                                                                                                                                56 TyrSerLeuValDhellePheGlyPheValGlyAsnMetLeuVallleLeulleLeulle
                                                                                  528 GGAAATACAATGTGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATC
SerGluProCysGlnLysIleAsnValLysGlnIleAlaAlaArgLeuLeuProProLeu
                                                                        108 AACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGAC
                                                                                                                      CTGTTTTTCCTTCTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCCAGTGGGACTTT
                                                                                                                                                                                                                                                                  648 TIAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGCT
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CRS provides that bind to CCRS, CCRS variants, and CCRS-binding agents capable of blocking membrane fusion between HIV and target cells represent potential anti-HIV therapeutics for macrophage tropic strains of HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288 TOGGAGCCCTGCCAAAAAACAATGTGAAGCAAATGGCAGCCGGCCCCTGCCTCGGCTC 347
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                                                                                                                                                                                                                                                                                                                                                                                                         It chemokine receptor 5 polypeptide - used to inhibit membrane fusion between \mbox{H\,{\sc i}}\mbox{V} and a target cell
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343
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Feng Y, Kennedy PE, Murphy PM;
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Matches:
Conservative:
Mismatches:
Indels:
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/note= "transmembrane domain"
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/note= "transmembrane domain"
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/note= "transmembrane domain"
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1768.50
96.36%
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CTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCCAGTGGGACTTTGGAAATACAATG
                                                                                                                                  CTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATGCTGTGTTTGCTTTAAAAGCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5), which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but not by moncyte chemoattractant protein 1 (MCP-1), MCP-3, MCP-3, interleukin e [II-9] or growth related gene product alpha (GRO alpha) chemokines. Active CCR-5 is also a receptor of human immunodeficlency virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can used to diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis, asthma, idiopathic pulmonary fibrosis and psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer, atherosclerosis and autoimmune disorders.
                                 Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention; inflammatory disease; rheumatofid arthritis; glomerulonephritis; asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer; atherosclerosis; autoimmune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Active and inactive forms of human CC chemokine receptor CCR-5 useful to diagnose, prevent and/or treat inflammatory disorders, autoimmune disease and viral infection
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Conservative:
Mismatches:
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1745.50
96.60%
96.32%
66.42%
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                                                                                                                                                         Homo sapiens
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     Human CCR5.
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1167 CIGCAAAIGCIGFICTATTICCAGCAAGAGGCICCCGAGCGAGCAAGCICAGTFTACAC 1226
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                                                                         CIGAAGAGCAIGACIGACAICTACCIGCICAACCIGGCCAICICIGAACIGITIIICCII 479
                                                                                                                    CTIACIGICCCCIICIGGGCICACIAIGCIGCCCCAGIGGGACIITGGAAAIACAAIG 539
                                360 TICATCITIGGITITIGIGGGCAACAIGCIGGICAICCICAICCIGAIAAACIGCAAAAGG 419
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                                Location/Qualifiers
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95US-0575967.
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N-PSDB; AAT85161.
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Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding agents capable of blocking membrane fusion between HIV and target cells represent potential anti-HIV therapeutics for macrophage
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                                                                chemokine receptor 5; CCR5; G-protein coupled receptor; an immunodeficiency virus; HIV; CD4; AIDS; therapy;
                                                                                                                                                                                                                                                          "extracellular loop-1 (Claim 19)"
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/note= "extracellular loop-3 (Claim 19)"
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                                     Human CC chemokine receptor 5 (CCR5).
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Feng Y, Kennedy PE, Murphy PM;
                                                                                                                                                                      Location/Qualifiers
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/label= I
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N-PSDB; AAT76920
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                                  serves as a correceptor for infection by macrophage tropic (M-tropic) strains of HIV-1. The invention relates to the identification of a CCR5 variant (see AAW88231), designated CCR5m303, comprising the first two transmembrane domains of wild-type CCR5, but lacking transmembrane domains 3-7. The presence of the CCR5m303 variant with the wild type CCR5 allele shows a positive correlation with resistance to infection with M-tropic HIV-1
                                                                                                                                                                                                                                                                              /note- "corresponds to TGT (Cys) in wild-type CCR5, TGA (Stop) in CCr5m303"
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                                                                                                                                                                             CCR5m303; co-receptor; infection; diagnosis; AIDS; human.
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strains, and may indicate slower progression of the disease. The detection of CCR5 variants may be used to identify individuals at lower risk of infection relative to the general population who, if infected, may exhibit slower progression to AIDS. Probes and primers (see AAV84127-36) are provided for use in diagnostic methods for detecting the presence of such variants. A method is provided for inhibiting HIV-1 infection a cell expressing the CCR5 receptor. This involves introducing a nucleic acid encoding a CCR5 variant into the cell, thereby reducing the number of functional CCR5 molecules present on the cell surface.
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                                                                GGTGACAGAGACTCTTGGGATGACGCACTGCTGCATCAACCCCATCATGTCTTTGT 1106
                                                                                                                                                     CCAGGAATTCTTTGGCCTGAATAATTGCAGTAGCTCTAACAGGTTGGACCAAGCTATGCA 1046
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                                                                                                                                                                                                                                                                                                                                                             inflammation; autoimmune disease; metastasis; bronchial asthma; lupus; chronic bowel inflammation; rheumatioid arthritis; cytostatic; antiliaflammatory; antiasthmatic; immunosuppressive; dermatological; antirheumatic; antiarthritic.
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identifying an agent which inhibits binding of a CCR5 ligand to a CCR5 receptor. The methods may be carried out in a subject, especially a human, infected (therapeutic method), not infected with HVV (prophylactic method), or in a subject who is not infected with, but has been exposed to, HIV.
                                                                                                                 Length:
Matches:
Conservative:
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                                                                                                                     Novel compounds comprising specific amino acids within CCR5 (HIV 1 co-receptor) amino terminal domain including negatively charged and two sulfated tyrosine residues is useful for treating HIV infection in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of human HIV-1 co-receptor CCR5.

Amino acids 2-18 in the N-terminal region of CCR5 comprise an HIV-1 pg120-pg120-bindings site that determines the specificity of the pg120-bindings site that determines the specificity of the interaction between CCR5 and HIV-1 gp120. Post-translational sulfation of the tyrosine residues in the CCR5 N-terminus is required for gp120 binding and may critically modulate the cusceptibility of target cells to HIV-1 infection in vivo. The invention provides claimed sulfated peptides (see AAB8247) that are based on the CCR5 N-terminal region and which are effective of inhibiting HIV-1 binding to CCR5. These peptides are used in claimed methods of inhibiting HIV infection of CD4+ cells, of preventing CD4+ cells from becoming infected with HIV, and of
                    GGTGACAGAGACTCTTGGGATGACGCACTGCTGCATCAACCCCCATCATGTCTTTGT
                                                      1107 CGGGGAGAAGTICAGAAACTACCTCTTAGTCTTCTTCCAAAAGCACATTGCCAAACGCTT
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                                                                                                                                                                                                                                                                                                                                   immunodeficiency virus type
anti-HIV-1.
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                                                                                                                                                                                                                                                                                                                                       co-receptor; human; therapy; vaccine;
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                                                                                                                                                                                                                                                                                                               Human HIV-1 co-receptor CCR5
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19-MAX-2000; 2000US-205839P.
07-FEB-2001; 2001US-267231P.
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N-PSDB; AAH26903.
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Binding-site
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nValThrGluThrLeuGlyMetThrHisCysCysIleAsnProlleIleTyrAlaPheVa 300	Pred. No.: Score:	SCOTES:
CGGGGGAGAAGTTCAGAAACTACTCTTAGTCTTCCAAAAGCACATTGCCAAACCCTT 1166 	Percent Simi Best Local S Query Match:	Percent Similarity: 96 Best Local Similarity: 96 Query Match: 66
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eCysLysCysCysSerIlePheGlnGlnGlnAlaProGluArgAlaSerSerValTyrTh 340	QY	240 ATGGATTATCAA
CCGATCCALTGEGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	qa .	
	č d	21 GlnLysileAsn
AAB83554 standard; Protein; 352 AA. AAB83554;	Qy.	360 TTCATCTTTGGT
09-OCT-2001 (first entry)	đ	41 PheilePheGly
CCR5 protein sequence.	δ. ξ	420 CTGAAGAGCATG
Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5; human immunodeficiency virus; anti-inflammatory disease; human.	i ko	480 CTIACTGTCCC
Homo sapiens.	qa	81 LeuThrValPro
EP1118858-A2.	QY	540 IGTCAACTCTT
25-JUL-2001.	qq	101 CysGlnLeuLeu
03-JAN-2001; 2001EP-0300020.	δy	600 CTCCTGACAATC
12-JAN-2000; 2000GB-0000659. 12-JAN-2000; 2000GB-0000661. 12-JAN-2000; 2000GB-0000663.	do Qy	121 LeuLeuThrile 660 ACGGTCACCTTT
PFIZER LID. PFIZER INC.	qa	
S, Perros M, Rickett GA;	δ <i>τ</i>	720 CTCCCAGGAATC
WFI; 2001-477088/52. N-PSDB; AAF87099.	55 AS	
Determining if an agent can modulate CCR5-gp120 interaction, comprises incubating the agent with CCR5 and gp120 and determining if the agent modulates the interaction	Db Qy	181 Hispheroryr 807 CTTGGGGCTGGT
Claim 1; Page 110; 113pp; English.	qa	200 eLeuGlyLeuVa
This sequence represents the human CCR5 protein sequence.	QY	867 TCTGCTTCGGTG
intion relates to a method for defermining whether an agent is of modulating the interaction of chemotactic chemokine receptor 5	QΩ	220 rLeuLeuArgCy
CCKS) With MPLAN, Comprising incommating the agent with Cox and Spize (CCKS) with Mother the agent modulates the interaction, where gpl20 is associated with CD4, and where the interaction is a low affinity CC binding. The method is used to identify an agent capable of modulating	Qy	927 CATGATTGTTPP
raction of CCR5 with gpl20. An agent identified by the method to prepare a pharmaceutical composition for the treatment of a corr condition associated with CCR5 and gpl20 interaction, to treat	Qy	987 CCAGGAAIICII
t with a disease or condition associated with CCR5 and gpl20	අු	260 eGinGluPheP
tions and to preparing a practice and to the control of the contro	δŏ.	1047 GGTGACAGAGAC
, and detects interaction of ani20 with cells expressing only	2	280 nValThrGluT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translocation of HIV into transformed mammalian cell or for identifying a human chemokine receptor that facilitates the infection of a particular HIV strain into the transformed mammalian cell. Compounds identified can be used to treat cellular dysfunction and to prevent or combat HIV infection. The present sequence is a human chemokine receptor (CRR), CC-CRR-5 related protein. CC-CRR-5 is the principal cofactor for entry mediated by the envelope giycoproteins of primary macrophage-tropic
                                           The present invention relates to a transformed mammalian cell that contains a gene encoding CD4, a construct encoding a reporter gene under the regulation of an human immuno deficiency virus (HTV) long terminal repeat (LTR) and that has been transduced with a vector encoding a human chemokine receptor (CKR) where the CD4 and the CKR are present on the cell surface of transformed mammalian cell. The invention is useful for identifying drugs or antibodies that interfere with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mammalian cell (I) that contains a CD4 gene, reporter gene for identification of drugs and antibodies for treatment of
                                                                                                                                                                                                                                                                                             Human; transformed mammalian cell; CD4; reporter gene; translocation; human immuod deficiency virus; HIV; long terminal repeat; LTR, therapy; chemokine receptor; CRR, cellular dysfunction; HIV infection; cofactor; CC-CKR-5; envelope glycoprotein; anti-HIV.
                                                                                                                                                                                                                                                                   Human chemokine receptor (CKR), CC-CKR-5 related protein #2.
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                                                                                                                rArgSerThrGlyGluGluGluIleSerValGlyLeu 352
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                                                                                                                                                                                    AAE04321 standard; Protein; 352 AA.
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19-JUN-1996;
19-MAY-1997;
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eCysLysCysSerIlePheGlnGlnGluAlaProGluArgAlaSerSerValTyrTh 340
                                                                                                                                                                                                                                                                                                                                 Human chemokine C-C motif receptor 5; CCR5; haplotype pair; isogene; single nucleotide polymorphism; SNP; human immunodeficiency virus 1; HIV-1 infection; acquired immunodeficiency syndrome; AIDS; antiviral; genotype; polymorphic variant; transgenic; drug screening; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New haplotypes of the human chemokine (C-C motif) receptor 5 gene, useful to diagnose and treat diseases associated with its abnormal expression or function, including human immunodeficiency virus-1
                                             CCGAICCACIGGGGAGCAGGAAAIAICIGIGGGCIIG 1263
                                                                                                                                                                                                                                                                                              Human chemokine (C-C motif) receptor 5 polypeptide.
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N-PSDB; ABA97318, ABA97319.
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CCAGGAATTCTTTGGCCTGAATAQTGCAGTAGCTCTAACAGGTTGGACCAAGGTATGCA 1046
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polymorphism; a recombinant non-human organism transformed with CCR5 polymucleotide expressing a CCR5 protein encoded by the variant sequence; an isolated antibody specific for the CCR5 polypeptide and a method for screening drugs targeting the CCR5 polypeptide.
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present sequence represents human CCR5.
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method for identifying a binding compound for CC chemokine receptor 5 (CCR5). The method involves screening a library of test molecules (particularly peptides) with immobilised CCR5, and then identifying those molecules which bind. The invention also relates to CCR5-binding molecules which bind. The invention also relates to CCR5-binding molecules identified using the method of the invention, methods for identifying consensus motifis for CCR5-binding peptides, a transfer vector encoding tagged CCR5, a computer-aided methods for determining the relative binding affinity of a test molecule to CCR5 and a computer aided drug screening assay that utilises the three-dimensional structure of CCR5. Compounds identified using the methods of the invention are useful for treating or preventing HIV (human immunodefliciency virus) infection or AIDS (acquired cimmunodefliciency syndrome) in a patient. The methods of the invention may also be used to identify agonists or antagonists of the interaction of CCR5 with its natural ligand, and to determine a binding motif for
                                                   1166
                                                                                                   CCR5; CC chemokine receptor 5; human; HIV infection; human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome; drug screening; identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying CC chemokine receptor 5 binding compound for treating AIDS, comprises binding a molecule from library to a molecule having binding property corresponding to CCR5 and identifying bound molecule -
                                                     CGGGGAGAAGTTCAGAAACTACCTCTTAGTCTTCTTCCAAAAGCACATTGCCAAACGCTT
                                                                                                                                                      CCGATCCACTGGGGAGCAGGAAATATCTGTGGGGCTTG 1263
                                                                                                                                                                 Hehir CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tan
                                                                                                                                                                                                                                                                                                    Human CC chemokine receptor 5 (CCR5).
                                                                                                                                                                                                                          AAM52828 standard; Protein; 352 AA.
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21-WAR-2010; 2000US-19129P.
20-WAR-2011; 2001US-0813444.
20-WAR-2001; 2001US-0813653.
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N-PSDB; ABA02317.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention provides isolated nucleic acid sequences that encode rabbit prostaglandin (EG) E2EP3 receptor, human PG E2EP2 receptor, human chemokine receptor CCR-5, human ss2 adrenergic receptor, human chemokine receptor CCR-5, human ss2 adrenergic receptor, rat renal outer medullary potassium ion channel protein or human small G-protein rho, cogether with deduced protein sequences. Also provided is a method for the production of eukaryotic proteins by culturing bacteria transformed with vectors contraining the above nucleic acid sequence on a nucleic acid (1) that comprising at least three positively charged amino acids, or a sequence comprising at least three positively charged amino acids, or a sequence comprising at least three positively charged amino acids, or a sequence combinant production of eukaryotic proteins, particularly membrane of, and in frame with, (ii) a sequence encoding a protein. (I) are used for recombinant production of eukaryotic proteins, particularly membrane proteins, G-protein coupled receptors or ion-channel proteins, in diagnostic and screening assays and as studies; as therapeutic agents; in diagnostic and screening assays and can immunohistochemical markers, e.g. for orphan receptors or ion channels. Antibodies raised against the chemokine receptors or ion channels. Antibodies raised against the chemokine receptor CCR-5 can be used (when administered as antiserum or generated in vivo) to prevent entry of human immune defliciency virus (HIV) into cells.
 1107 CGGGGAGAAGTICAGAAACTACCICTIAGICTICCIAAAAGCACATIGCCAAACGCTI 1166
                                                             chemokine receptor; ss2 adrenergic receptor; small G-protein rho; renal outer meduliary potassium ion channel protein; ion-channel protein; lambda phage repressor protein; G-protein coupled receptor; bacteria; biochemical; vaccine; immunohistochemical; orphan receptor; HIV.
                                                                             New nucleic acid constructs for high level expression of eukaryotic proteins in bacteria, for producing e.g. chemokine receptor CCR-5 for
                                                                                                                                                                                                                                                                                                                                           Prostaglandin; PG; E2EP3 receptor; E2EP2 receptor; CCR-5; human;
                                                                                                                                                                                                                                                                                                                 Fusion protein containing human chemokine receptor CCR-5.
                                                                                                                             CCGATCCACTGGGGAGCAGGAAATATCTGTGGGCTTG 1263
                                                                                                                                           Disclosure; Page 49-53; 81pp; English.
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                                                                                                                                                                                                                                                                                  (first entry)
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CCAGGAATTCTTTGGCCTGAATAATTGCAGTAGCTCTAACAGGTTGGACCAAGCTATGCA 1046
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                                                                  PhellephedlyPheValGlyAsnMetLeuValIleLeuIleLeuIleAsnCysLysArg
                                                160 ITCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGG
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                                       378 IGlyCluLysPheArgAsnTyrLeuLeuValPhePheGlnLysHisIleAlaLysArgPh 398
                                                  The invention relates to G protein-coupled receptors (GPCRs) for which the endogenous ligand has been identified. Non-endogenous constitutively activated versaions of known GPCRs are used in the invention for the direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists. Such associated with GPCRs. The present sequence is a non-endogenous version of a known human GPCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 use in
CGGGGAGAAGTTCAGAAACTACCTCTTAGTCTTCCTTCCAAAAGCACATTGCCAAACGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying agonists of G protein-coupled receptors (GPCRs) for u disease treatment, comprises contacting candidate compounds with versions of GPCRs
                                                                                                                                                                                                                           Human; G protein-coupled receptor; GPCR; non-endogenous; mutant; constitutively activated GPCR; agonist; disease.
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                                                                                 CCGATCCACTGGGGAGCAGGAAATATCTGTGGGCTTG 1263
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                        Non-endogenous human GPCR protein, SEQ ID NO: 477
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                                                                                                                                             ABB56342 standard; Protein; 352
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1739.50
96.32%
96.03%
66.19%
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                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                           (AREN-) ARENA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                               Lehmann-Bruinsma K,
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Best Local Similarity:
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CCAGGAATICITIGGCCIGAATAATIGCAGIAGCICIAACAGGIIGGACCAAGCIAIGCA 1046
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                              ATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method for identifying a binding compound for CC chemokine receptor 5 (CCR5). The method involves screening a library of test molecules (particularly peptides) with immobilised CR5, and then identifying those molecules which bind. The invention also relates to CCR5-binding molecules which bind. The invention also creates to CCR5-binding molecules identified using the method of the invention, methods for identifying consensus motifs for CCR5-binding peptides, a transfer vector encoding tagged CCR5, a computer-aided pethods for determining the relative binding assay that utilises the computer aided drug screening assay that utilises the three-dimensional structure of CCR5. Compounds identified using the chaman immunodeficiency virus) infection or AIDS (acquired immunodeficiency syndrome) in a patient. The methods of the invention of immunodeficiency syndrome) in a patient. The methods of the interaction of CCR5. The present sequence represents a naturally occurring variant of human CCR5. The present sequence represents a naturally occurring variant of human cCR5 in which there is a glutamine, rather than a leucine, at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying CC chemokine receptor 5 binding compound for treating AIDS, comprises binding a molecule from library to a molecule having binding property corresponding to CCR5 and identifying bound molecule -
                                                                                          CCR5; CC chemokine receptor 5; human; HIV infection; human immunodeficiency virus; ALDS; acquired immunodeficiency syndrome; drug screening; identification; variant.
                                                                                                                                                                                                               /note= "Glu replaces wild-type Leu; encoded by CTG"
58
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339
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12
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                               /note= "Encoded by AGC"
                                                                                                                                                                                       Location/Qualifiers
55
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2000US-191299P.
2001US-0813448.
2001US-0813651.
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96.03$
66.19$
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                                                                                                                                                                                                                                                                                                                                                              21-MAR-2001; 2001WO-US09155
                                        (first entry)
                                                                      Human CCR5 Gln 55 variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nestor JJ, Wilson CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-010610/01.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABA02318.
                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                               WO200171346-A2
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21-MAR-2000; 2
20-MAR-2001; 2
20-MAR-2001; 2
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Pred. No.:
                                        22-FEB-2002
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                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                               27-SEP-2001
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        AAM52829;
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DB:
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The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10 protein. CCR5 HDGNR10 antibodies are useful for treating, preventing cor ameliorating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells, HIV infection (such as pneumocystis carini) pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen presenting cell interaction. The disease or disorder may also be an infection a cytomegalovirus infection such as an early stage HIV infection, a cytomegalovirus infection, or a poxvirus infection, an autoimmune disease (e.g. rheumatoid arthritis) or a pervirus infection, an autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The disease or disorder may be associated with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5 ingend expression, lack of CCR5 ingend function. CCR5 HDGNR10 protein classed as a food additive or preservative to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome diagnosis, treatment and prevention of cancer (breast, ovari, aberrant control protein, and provention of cancer (breast, ovari, aberrant control protein, and prevention of cancer (breast, ovari, aberrant control protein, and provention of cancer (breast, ovary, adrenal protein) and by a marrow casterial protein, and the marrow casterial protein and the protein casterial protein and the prevention of cancer (breast, ovary, addrenal protein) and the protein casterial protein and the protein casterial protein and the protein casterial protein are also useful in the casterial protein and the protein casterial protein are protein and the protein and the protein and the protein are also useful in the casterial protein and the protein are also casterial protein and the protein are also casterial protein and the protein and th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy; eurordegenerative disorder; Raposi's sarcoma; autoimmune disease; rheumatoid arthritis; concer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; menitiple sclerosis; ulcerative colitis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gastrointestinal tract, liver, lung,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
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                                                                                                                   AAE07039 standard; Protein; 352 AA.
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09-MAR-2000; 2000US-0187999.
22-SEP-2000; 2000US-0234336.
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N-PSDB; AAD13198.
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RESULT 15
AAE07039
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AA; 352

Sequence

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1107 CGGGGAGAAGTICAGAAACTACCTCTTAGTCTTCCTAAAAGCACATTGCCAAACGCTT 1166
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      Length:
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"Genomic Organization and Functional Characterization of the Complete "Genomic Organization and Functional Characterization of the Complete Receptor Organization Unit for the Chemokine Receptor CCR-5, a Major Entry Co-Submitted (JOH HIV).";

EMBL, AF009962; AAC23944.1; -.
EINEFPRO; IPR000756; GPCR_Rhodpsn.
Pfam; PF0001; 7tm_1; 1.
PROSITE; PS00037; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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-Q-/cgn2_1/USPTO_spool/US09938703/runat_03062003_161407_22827/app_query.fasta_1.1870
-Q-/cgn2_1/USPTO_spool/US09938703/runat_03062003_161407_22827/app_query.fasta_1.1870
-DB=SPTREMBL_21 -QFWT=fastan -SUFETX=rspt - MANACH=0.1 -LOOPCL=0 -LOOPCL=0
-UNITS-blits -START=1 -END=-1 -MATLEND=0 -TRANS=human40.cdl -LISS=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MXX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTEMT=pto -NORM=ext -HEAPSIZE=500 -MINIER=0 -MAXIEN=200000000
-USRE-SEG9938703_cccN_1_1132_erunat_0306203_161407_22827 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LOMGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -PHERRANS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDOP=6 -DELEXT=7
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                          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Query Match:

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2 ITAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTCG 61
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Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,

Edo D.,

Library L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,

Ho D.D.,

ALDS Res. Hum. Retroviruses 0:0-0(1997).

ALDS Res. Hum. Retroviruses 0:0-0(1997).

EMBL, ARB65704.11 .

PFRONIC: PROMO0276, GPECR. Rhodpsn.

PRIME: PROMO01; 7tm_1; 1.

PROMITE: PROMO177; GPERRHODOPSN.

PROSITE: PROMO277; GPERRHODOPSN.

PROSITE: PSO0237; G_PROTEIN. RECEP_F1_1; UNKNOWN_1.
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                                                                                                                            Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID-9606;
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF161913: AAD47670.1;
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam: PF00001; 7tm_1; 1.
PRINTS; PR000237; GPCRHODOPSN.
PROSITE; PS00237; G_PROTEIN.RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN.RECEP_F1_2; 1.
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39183 MW; 56C819F92D6DB1A6 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 17, Last annotation update)
C-C chemokine receptor 5 (Fragment).
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Matches:
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MEDLINE-99392755; PubMed-10465086;
Aikhionbare F.O., Newman C., Womack C., Roth W.W., Stringer H.G. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AIDS 13:1585-1586(1999).
                                      3C9146C76BA416F7 CRC64;
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60 AA; 7156 MW; AFF4B9CAF6B80AFB CRC64;
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01-OCT-2000 (TEMBLRel. 15, Last sequence update)
01-JUN-2001 (TEMBLRel. 17, Last annotation update)
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PROSITE; PS02062; G_PROTEIN_RECEP_F1_2; 1.
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01-MAY-2000 (TIEMBLRel. 13, Last sequence update) 01-JUN-2001 (TIEMBLRel. 17, Last annotation update)
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFIG1944, AAD47671.1;
PINTERPONDIST, FRENDORSN.
PRANTS, PRODOST; GPCR-Rhodpsn.
PROSTIE: PS00237; GPCR-RHODPSN.
PROSTIE: PS00237; GPCR-RHODPSN.
PROSTIE: PS00237; GPCR-RHODPSN.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID=9606;
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339 AA, 39086 MW, 88AD8B44E2CB4EC2 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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                                             Pred. No.:
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Q9UN27
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2 TTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTCG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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                                                                                                                                                                                                       ×.;
                                                                                      Craniata; Vertebrata; Buteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                              SEQUENCE FROM N.A.
Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.
"Sequences of the CCR5 genes from diverse simian and prosimian species.";
                                                                                                                                                                                                                                                                                      Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF161916; AAD47673.1; -
InterPro: IPR000276; GFCR_Rhodpsn.
Pfam; PF00017; THL.1.
PRIMTS: PR000237; GFCREHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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01-MAY-2000 (ITEMBLrel. 13, Last sequence update)
01-UNY-2001 (ITEMBLrel. 17, Last annotation update)
C-C chemokine receptor 5 (Fragment).
CCR5.
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InterPro; IPR000276; GPCR_Rhodpsn.
PR1MTS; PR00037; GPCRRHODOSN.
PROSITE; PS00237; GPRRHODOSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Matches:
Conservative:
Mismatches:
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01-JUN-2001 (TrEMBLrel. 17, Last ann C-C chemokine receptor 5 (Fragment).
                                                                                   Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
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152.00
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                                                                    Homo sapiens (Human)
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Best Local Similarity:
Query Match:
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(Human)
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                                                                                        Homo sapiens
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SEQUENCE
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Q9UBT9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kulken C., Marx P., Wolinksy S.;
"Sequences of the CCR5 genes from diverse simian and prosimian
apecies.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AE161919; AAN47676.1; -
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRNTS; PR00237; GPCRHODOPSN.
PRNSTS; PS00237; G_PROTEIN.RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN.RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8BAF02E19423BF79 CRC64;
10FE05FE5371D4B3 CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
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                                                                                                                                                                                                                                                                                                               209 GlylleLeulysThrLeuLeuArgCysArgAsn 219
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Matches:
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339 AA; 39066 MW;
 39146 MW;
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   339 AA;
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Best Local Similarity:
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Q9UN23;
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2 TIAAAGATAGICATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTCG 61
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SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,

"Sequences of the CCR5 genes from diverse simian and prosimian
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Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID-9606;
                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161915; AAD47672.1; -
EMBL; AF161909; AAD47665.1; -
EMBL; AF161910; AAD47667.1; -
EMBL; AF161911; AAD47668.1; -
EMBL; AF161912; AAD47668.1; -
EMBL; AF161912; AAD47689.1; -
EMBL; AF161912; AAD47689.1; -
EMBL; PR000177 Tm.1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                               species.;
Submitted (ULI-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF161920; AAD47677.1;
InterPro: IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRNTKS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPCRHODOPSN.
PROSITE; PS00237; G_PROTEIN.RECEP_F1_1; UNKNOWN_1.
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339 339
339 AA; 39115 MW; 3C6369F922C91AA7 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 17, Last annotation update)
C-C_Chemokine receptor 5 (Fragment).
01-MAY-2000 (TrEMBirel. 13, Created)
01-MAY-2000 (TrEMBirel. 13, Last sequence update)
01-MAY-2000 (TrEMBirel. 17, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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2 TTAAAGATAGTCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTCG
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                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Kurber B., Oprondek J., Stanton J., Agy M., Kunstman K., Chen Z., Rorber B., Oprondek J., Marx P., Wolinksy S., Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hylobates concolor (crested gibbon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Butheria; Primates; Catarrhini; Hylobatidae; Hylobates.
                                                                                                                                                                                                                            Hylobates concolor (crested gibbon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  species.";
Dubmitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AE161888; AAD47645.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      339 AA; 39075 MW; 09257FBFB834C4AE CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                         01-WAY_2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF161887; AAD47644.1; -...
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PR00017; 7tm_1; 1.
PRINTS; PR000237; GPCRAPIODESN.
PRINTS; PR000237; GPROTEIN RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Matches:
Conservative:
Mismatches:
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209 GlylleLeuLysThrLeuLeuArgCysArgAsn 219
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enkaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF161921; AAD47678.1; --
EMBL, AF161917; AAD47678.1; --
INTERPROJOUST (SPCR_Rhodpsn.)
Fram: PPROJOST; GPCR_RHODPSN.
PRINTS; PROJOST; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
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                                                                                                            339 AA; 39114 MW; 3C6369F92C29F4A7 CRC64;
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01-MAY-2000 (TTEMBLRel. 13, Last sequence update)
01-UN-2001 (TTEMBLRel. 17, Last annotation update)
C-C chemokine receptor 5 (Fragment).
    PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1. PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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A; 39128 MW;
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCR5 genes from diverse simian and prosimian
species."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
NCBL_TaxID-29089;
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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Interpro; IPR000276; GPCR_Rhodpsn.
PRAM: PR00031; 7tm.1; 1.
PRINTS; PR000237; GPCRRHODOPSN.
PROSTIE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
Pfam; PP00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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SEQUENCE 339 AA; 39024 MW;
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Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                      Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
"Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                  species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, API61899; AAD47656.1;
InterPro; IRR000276; GPCR_Rhodpsn.
Pfam; PR00001; 7tm_11: 1.
PRNTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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339 AA; 39157 MW; 4A9EBAD183E8E72D CRC64;
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01-MAY-2000 (WIEMBLIEL: 13, Last sequence update)
01-JUN-2001 (WIEMBLIEL: 17, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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-!- FUNCIION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIP-1-BETA AND RAWTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-UTL-1998 (Rel. 36, Created)
15-UTL-1998 (Rel. 36, Last sequence update)
16-OTL-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5)
CCR5 OR CMKBR5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Kidney;
MEDITIE-9800187; PubMed-9343222;
MEDITIE-9800187; PubMed-9343222;
"Numann S.E., Platt E.J., Kozak S.L., Kabat D.;
"Polymorphisms in the CCR5 genes of African green monkeys and mice implicate specific amino acids in infections by simian and human limmunodeficiency viruses."

J. virol. 71:8642-8656(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cercopitherms aethiops (Green monkey) (Grivet).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murayama Y., Matsunaga S., Inoue-Murayama M.; "CDNA sequence of African green monkey CCR-5 chemokine receptor
                                                                                                                     P51675
P51679
P35411
Q920d9
P51676
O18983
                                                                                                                                                                                                                             09xt45
P51680
                                                                                                                                                                                                                                                                                                                                                                                                                                              352 AA.
                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                              C3X1_RAT
C3X1_MOUSE
CKRV_MOUSE
                                                                                                                                                                                                                CCR6_MACNE
                                                                                                                                                                                                                                                                                                                        CKR6_HUMAN
                                                   MACMU
CERAE
HUMAN
                                                                                                                                                                                      CERAE
                                                                                                                     MOUSE
                                                                                                                                   HUMAN
                                                                                                                                                                                                     HUMAN
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                                                                                                                                                                                                                                                                                  SPVKA
                                                                                                                                                                                                                                                                                               CKR7_HUMAN
                                                                                                                                                                                                                                                                                                             CKR8_HUMAN
                                                                                                                                                                                                                                            MOUSE
                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cercopithecinae; Cercopithecus.
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NCBI_TaxID=9534;
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gene.";
  -MODEL-frame-inp.model -DEV-x1p
-MODEL-frame-inp.model -DEV-x1p
-MODEL-frame-inp.model -DEV-x1p
-MODEL-frame-inp.model -DEV-x1p
-Q-<qn, 21/USFVC-pool/10809393F03/runat_03062003_161406_22808/app_query.fasta_1.1870
-DE-S418SPC-t_40 -GPMT-fastan -SUFFTX-rep -MINAXCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-blts -START-1 -END-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45
-UNITS-blts -START-1 -END-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45
-UNITS-blts -START-1 -END-1 -MATRIX-0 -ALIGN-15 -MODE-LOCAL
-UNITS-pto -NORM-ext -HEAPSIZE-500 -MINIEM-0 -MAINEN-200000000
-USER-US09938703_eCGN_1 1_38_erunat_03062003_161406_22808 -NCPU-6 -ICPU-3
-NO_MAR -LARGOURRY -MES_SCORES-0 -WAIT -DSPBLCOR-100 -LONGIAG
-DEV_TIMEOUT--10 -WARN_ILMEDOUT--30 -THEREDS-1 -XGARPOR-10 -XGARPEXT-0.5 -FCARPOR-6
-FGAREXT-7 -YGAROP-10 -YGARDEXT-0.5 -DELDOR-6 -DELEXT-7
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macaca mula
macaca mula
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5096.611 Million cell updates/sec
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                                                                                                                                                                          1 ATTAAAGATAGTCATCTTGG......CTCTGCTTCGGTGTCGAAAT 94
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                                                                                               June 3, 2003, 18:39:54 ; Search time 1.52995 Seconds
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                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                       nucleic - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                 fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                     112892 seqs, 41476328 residues
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CKR5_MOUSE
CKR3_MOUSE
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CKR5_PANTR
CKR5_PAPHA
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CKR5_PYGNE
CKR5_MACMU
                                                                                                                                                     US-09-938-703-3_COPY_792_885
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Maximum Match 100%
Listing first 45 summaries
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Yqapop 10.0 , Yqapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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133
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Database :

No. Result

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Primary SIVsm isolates use the CCR5 coreceptor from sooty mangabeys
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062743; 062744; 062745; 062746;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5).
                                                                     PRINTS; PRO0237; GPCRREDDOPSN.
PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cercocebus torquatus atys (Red-crowned mangabey). (Sooty mangabey). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
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SULFATION (BY SIMILARITY).
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Mismatches:
Indels:
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                                            EMBL; AB015944; BAA31328.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                 40561 MW;
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                            EMBL; U83324; AAC51795.1; -. EMBL; U83325; AAC51796.1; -.
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                                                                                                   -I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, MIP-1-BETA AND RANTES AND SUBSCIBENT TRANSDICES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEYEL. MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
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comparison of coreceptor usage
                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Y -> D (IN ISOLATE 087).
V -> G (IN ISOLATE 087).
M -> K (IN ISOLATE 089).
L -> V (IN ISOLATE 089).
V -> G (IN ISOLATE 089).
V -> L (IN ISOLATE 089).
T -> I (IN ISOLATE 099).
T -> I (IN ISOLATE 099).
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Mismatches:
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Matches:
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   naturally infected in west Africa; a cc
of primary SIVsm, HIV-2, and SIVmac.";
Virology 246:113-124(1998).
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EMBL; AF051903; AAC39831.1; -.
EMBL; AF051904; AAC39832.1; -.
EMBL; AF051905; AAC39833.1; -.
Interpro; IPR000276; GPCR_Rhodpsn.
Pfan; PF00001; 7tm.1; 1.
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                                                                                                                                                                                                                                                                                                                MEDLINE-97286687: PubMed-9108095; Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M., Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M., Edinger A.L., Amedee A., Miller K., Doranz B.J., Murphey-Corb M., Pelper S.C., Parmentier M., Broder C.C., Doms R.W.; Ediferential utilization of CCR5 by macrophage and T cell tropic pind inmunodeficiency virus strains. "Differential utilization of CCR5 by macrophage and T cell tropic proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).

-i- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCLUM IONS LEVEL. MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
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EMBL, PR005629, AAB62553.1; -.

InterPro; IPR0000216, GECR_Rhodpsn.

PRIMES, PR00237, GEPROREIN RECEP_F1_1; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmentane; Glycoprotein; Sulfation.

G-protein coupled receptor; Transmentane; Glycoprotein; Sulfation.
                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
CCR5 OR CMKBR5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SUBCELLUIAR LOCATION: Integral membrane protein.
-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                    Gorilla gorilla gorilla (Lowland gorilla).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
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EXTRACELLULAR (POTENTIAL).

CYOPILSHIAL).

CYOPILSHIC (POTENTIAL).

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EXTRACELLULAR (POTENTIAL).
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7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                GlylleLeuLysThrLeuLeuArgCysArgAsn 226
                   GGAATCCTAAAAACTCTGCTTCGGTGTCGAAAT 94
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CALGOS; 014693; 014695; 014696; 014697; 014699; 014700; 014701; 014702; 014702; 014702; 014702; 014702; 014707; 014706; 014707; 014700; 014701; 014702; 014707; 014706; 014707; 016702-1996 (Rel. 34, Created)
CAT-1996 (Rel. 34, Last sequence update)
15-UNL-2002 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR-5) (HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).
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MEDLINE-98010187; PubMed-9343222;
KLUDMAND S.E., Platt E.J., Kozak S.L., Kabat D.;
"Polymorphisms in the CCR5 genes of African green monkeys and mice implicate specific amino acids in infections by simian and human immunodeficiency Yiruses.";
J. Yirol. 71:8642-8656(1997).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,

McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,

Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,

Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,

Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,

Porcel B.M., Dragan Y., Glacalone J., Pae A., Powell E.,

Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,

Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;

Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.; "Cloning and functional expression of CC CKR5, a human monocyte chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96241590; PubMed-8639485; Sanson M., Labbe O., Mollereau C., Vassart G., Parmentier M.; *Molecular,cloning and functional expression of a new human
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                                        Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC-chemokine receptor gene.";
Biochemistry 35:3362-3367(1996).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                               MEDILINE-98049523; PubMed-9388201; Minmidi S., Ahuja S.K.; McDaniel B.L., Ahuja S.K.; McDaniel B.L., Ahuja S.K.; Thuman CC chemokine receptor 5 (CCR5) gene. Multiple transcripts with 5'-end heterogenelty, dual promoter usage, and evidence for polymorphisms within the regulatory regions and noncoding exons."; J. Biol. Chem. 272:30662-30671(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,
Gerard N.P., Gerard C., Sodroski J., Choe H.;
Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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                                                                            HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism."; AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE-96260018; PubMed-8649512;
Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,
                                                                                                                                                                                                                                                                                                                                                                        MEDILINE-9626017; PubMed-8649511;
Deng H., Liu R., Ellmeler W., Choe S., Unutmaz D., Burkhart M.,
Deng H., Liu R., Ellmeler W., Choe S., Unutmaz D., Burkhart M.,
Della Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,
Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
*Identification of a major co-receptor for primary isolates of
                                                                                                                                                                                                                                                                                    Magierowska M., Barre-Sinoussi F., Issafras H., Theodorou I.,
                                                                                                                                                                                                                                                                                                                     Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
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[6] SEQUENCE FROM N.A., AND POLYMORPHISMS.
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                                MEDLINE-98022612; PubMed-9359654;
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cell 96:667-676(1999).
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U95626; AAB57793.1; -. U83326; AAC51797.1; -.

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PROSITE; PS00237; G_PROTEIN_RECEP_R1_1; 1. BROSITE; PS50262; G_PROTEIN_RECEP_R1_2; 1. G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation; Polymorphism.
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EXTRACELLULAR (POTENTIAL).
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A -> S (IN DBSNP:1800939).
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R -> H (IN INCCR5-72A).
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EXTRACELLULAR (POTENTIAL).
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Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
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AAB65731.1;
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AF011536; AAB65736.1;
AF011537; AAB65737.1;
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2 TTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTCG 61
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCK5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE-97426118; PubMed-9282822;
Zacharova V., Zachar V., Goustin A.S.;
"Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEGUENCE FROM N.A.
MEDLINE-97268687; PubMed-9108095;
Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
"Differential utilization of CCRS by macrophage and T cell tropic
Sinfan immunodeficiency virus strains.";
Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism."; AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
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MEDLINE-98090115; PubMed-9430250;
MEDLINE-98090115; PubMed-101200;
MEDLINE-98090115; PubMed-9430250;
MEDLINE-080115; PubMed-9430250;
MEDLIN
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              7 (POTENTIAL).
CYTOPLASHIC (POTENTIAL).
BY SIMILARITY.
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
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Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
  EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                       US-09-938-703-3_COPY_792_885 (1-94) x CKR5_HYLLE (1-352)
                                                                                                                                                                                                Length:
Matches:
Conservative:
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AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
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                                                                                                                                                                                                                                                          Mismatches:
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MEDLINE-98022612; PubMed-9359654;
                                                                                                                                       40445 MW;
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Pan troglodytes (Chimpanzee).
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352 AA;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                  Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
"Sequence evolution of the CCR5 chemokine receptor gene in primates.";
Mol. Blol. Evol. 16:1145-1134(1999).
-I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 3), Last sequence update)
15-JUN-2002 (Rel. 4), Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hylobates leucogenys (White-cheeked gibbon).
Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhinl; Hylobatidae; Hylobates.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 (POTENTIAL).
EXPRACELLUIAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                               Conservative:
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Indels:
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                                     Length:
Matches:
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                                   5.57e-14
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SEQUENCE FROM N.A.
                                                                                                Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCR5 OR CMKBR5.
                                                                               Percent Similarity
                    Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 TTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTCG 61
BINDS TO MIP-1-ALPHA,
        MIP-I-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein: SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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4A33E698B80FE34C CRC64;
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Matches:
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interPro; IPR000276; GPCR_Rhodpsn.
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EMBL; U94329; AAB58446.1; -.
EMBL; AF011342; AAB65742.1; -.
EMBL; U97666; AAC51670.1; -.
EMBL; AF011540; AAB65740.1; -.
EMBL; U89797; AAC03717.1; -.
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ID CKR5_PAPHA
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEYEL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
                                                                                                                                                                                                                                                                                                                                                                                                                   Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.; "Species-specific changes in the CCR5 gene from African and Asian nonhuman primates.";
          15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
16-OUL-2011 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
CCR5 OR CMKBR5.
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN 1 30 EXTRACELBUIAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                     SPECIES-P. hamadryas;
MEDLINE-97266687; PubMed-9108095;
Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Edinger A.L., Amedee A., Miller K., Clements B.J., Endres M.,
Peiper S.C., Parmentier M., Lu Z.H., Clements J.E., Murphey-Corb M.,
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
Pifferential utilization of CCRS by macrophage and T cell tropic
Sintan immunodeficiency virus strains.";
Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                           Papio hamadryas (Hamadryas baboon), and
Papio anubis (Olive baboon).
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MEDLINE-99210133; PubMed=10195758;
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EMBL; AF105287; AAD20556.1; ~.
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                                                                                                          (Olive baboon).
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NCBI_TaxID=9557, 9555;
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EXTRACELLULAR (POTENTIAL)

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261
278
302
101
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ID CKR5_PYGBI
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                                                                                                                                                                                                                                                                       2 ITARAGATAGICATCITIGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTCG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang Y.-W., Ryder O.A., Zhang Y.-P.;

"Sequence evolution of the CCR5 chemokine receptor gene in primates.";

Mol. Biol. Evol. 16:1145-1154(1999).

-!- FUNCTION: RECEPTOR FOR A CC TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,

MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY

INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE

IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR000276; GPCR_Rhodpsn.
Pfam: PF00001; 7tm_1: 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_FL_1: 1.
PROSITE; PS50262; G_PROTEIN_RECEP_FL_2: 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SUBCELLUIAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pongo.
NCBL_TaxID=9600;
                                                                                                          N-LINKED (GLCNAC. . .) (POTENTIAL). 5E1504A9BA1FE8B2 CRC64;
                                                    BY SIMILARITY.
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
                     EXTRACELLULAR (POTENTIAL)
                                 7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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31
0
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                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                   216 GlylleLeuLysThrLeuLeuArgCysArgAsn 226
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MEDLINE-99416438; PubMed=10486970;
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92.68%
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                                                                                                                        352 AA;
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219
236
261
261
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                                                                                                                                               Alignment Scores:
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CARBOHYD
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CKR5_PONPY
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDILINE-99416438; PubMed-10486970;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Sequence evolution of the CCR5 chemokine receptor gene in primates.";
Mol. Biol. Evol. 16:1154(1999).
-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEYEL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
Pygathrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-CKR-5) (CCR5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCR5 OR CMKBR5. Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti)
                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                       CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Mismatches:
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DIFFERENTIATION.
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Best Local Similarity:
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THE CONTROL OF GRANDLOCYTIC LINEAGE PROLIFERATION OR
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097879;
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entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDILINE-99416438; PubMed=10486970;

Zhang Y.-W., Ryder O.A., Zhang Y.-P.;

Sequence evolution of the CCR5 chemckine receptor gene in primates.";

Mol. Biol. Evol. 16:1145-1154(1999).

-I- FUNCTION: RECEPTOR FOR A CC TYPPE CHEMCKINE. BINDS TO MIP-1-ALPHA,

MIP-1-BETA AND RANTES AND SUBSEQUENTY TRANSDUCES A SIGNAL BY

INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosfomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 4). Last amortation update)
C-C_chemokine_receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5).
                                                                                          Transmembrane; Glycoprotein; Sulfation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trachypithecus francoisi (Francois' langur) (Indochinese langur).
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EXTRACELLULAR (POTENTIAL).
                                                                                                    EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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JLEATION (BY SIMILARITY)
JLEATION (BY SIMILARITY)
4366F142730F938F CRC64;
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
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                                                                                                                                                       3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Matches:
Conservative:
Mismatches:
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                                                                                                                                   (POTENTIAL).
                                      InterPro; IPR000276, GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPRRADODSN.
PROSITE: PS00237; G_PROTEIN_RECEP_FL_1; 1.
PROSITE: PS02026; G_PROTEIN_RECEP_FL_2; 1.
G-protein coupled receptor; Transmembrane;
                                                                                                                                                                                                 (POTENTIAL)
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152.00
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92.68%
                               EMBL; AF075445; AAD19857.1;
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                                                                                                               58
89
89
1102
1104
1106
1108
2235
2335
178
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NCBI_TaxID=54180;
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125
142
167
199
219
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Bukaryota; Metazoa; Chordata; Craniata; Veriebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
Trachypithecus.
                                                                                                                                                                                                                EMB: AR075442; AAD19554.1; -.
EMB: AR075442; AAD19554.1; -.
EMB: AR00217; GPCR_Rhodpsn.
Pfan: PF00001; 7tm.1; 1.
PROSITE; PS00237; GPCRRHODOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G_PROTOCION COUPLED TRANSMEMBRANE; GLYCOPROTEIN; Sulfation.

G_PROTOCION SULFACELLULAR (POTENTIAL).
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30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
CCR5 OR CMKBR5.
SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
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SULFATION (BY SIMILARITY).
4366F148C255938F CRC64;
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Conservative:
Mismatches:
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                              Zhang Y.-W., Ryder O.A., Zhang Y.-P.; "Sequence evolution of the CCR5 chemokine receptor gene in primates."; Mol. Biol. Evol. 16:1145-1154(1999).
                                                                                                                                                                                                                                     - FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, MIP-1-BETA AND RANTES AND SUBSCIDENTY TRANSDOESS A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
                                                                                 Pygathrix nemaeus (Dove langur).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                          30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; TPR000276; GPCR_Rhodpsn.
Pfan; PF0001; 7tm_1; 1.
PRINTS; PR00237; GPCRHODDSN.
PROSITE; PS00237; G_PROTEIN_RECEP_FI_1; 1.
PROSITE; PS00263; G_PROTEIN_RECEP_FI_2; 1.
PROSITE; PS00263; G_PROTEIN_RECEP_FI_2; G]ycoprotein; Sulfation.
DOMAIN 1 30 EXTRACELLUIAR (POIENTIAL).
                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
FE4F9D9BD3B3E861 CRC64;
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6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Mismatches:
Indels:
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MEDLINE=99416438; PubMed=10486970;
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40532 MW;
             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seq
15-JUN-2002 (Rel. 41, Last ann
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Query Match:
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NCBI_TaxID=54133;
                                                                       CCR5 OR CMKBR5
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                                                        Zhang Y.-W., Ryder O.A., Zhang Y.-P.;

"Sequence evolution of the CRS chemokine receptor gene in primates.";

Mol. Biol. Evol. 16:1145-1184 (1999).

-I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,

MIP-1-BETA AND RANTES AND SUBSEQUENTIX TRANSDUCES A SIGNAL BY

INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE

IN THE COMTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
                                                                                                                                                                    -i- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane, Glycoprotein; Sulfation. EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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Mismatches:
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Matches:
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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INTERPRO; IPR000276; GPCK_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                               SEQUENCE FROM N.A. MEDLINE-99416438; PubMed=10486970;
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Best Local Similarity:
  NCBI_TaxID=61618;
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CKR2_MACMU
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simian immunodeficiency virus strains.";
Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANPES SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCLUM IONS LEVEL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
                                                                                                                                 P79436; 002746;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 41, Last annotation update)
15-UNN-2002 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
"Genetically divergent strains of simian immunodeficiency virus use CCR5 as a coreceptor for entry.";
J. virol. 71:2705-2714(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                  Macaca mulatta (Rhesus macaque),
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
Macaca nemestrina (Pig-tailed macaque)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE-21354176; PubMed=11461684; Margulies B.J., Hauer D.A., Clements J.E.; Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M., Sharton M., Samson M., Iu Z.H., Clements J.E., Murphey-Corb M., Petiper S.C., Parmentier M., Broder C.C., Doms R.W.;
*Differential utilization of CCR5 by macrophage and T cell tropic
                                                                                                                                                                                                                                                                                                                                       MEDLINE-97184592; PubMed-9032394;
Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L., Newman W., Gerard N., Gerard C., Sodroski J.;
"Utilization of C-C chemokine receptor 5 by the envelope 91ycoproteins of a pathogenic simian immunodeficiency virus, SIVmac239.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
MEDLINE=97268687; PubMed=9108095;
                                                      62 GGAATCCTAAAACTCTGCTTCGGTGTCGAAAT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIDS Res. Hum. Retroviruses 17:981-986(2001).
                                                                                                                       352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SPECIES-M.mulatta; STRAIN-Indian macaque;
MEDLINE-97213934; PubMed-9060623;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Virol. 71:2522-2527(1997).
                                                                                                                                                                                                                                                                                       Cercopithecinae; Macaca.
NCBI_TaxID=9544, 9541, 9545;
                                                                                                                         STANDARD;
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                                                                                                                                                                                                        CCR5 OR CMKBR5.
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                                                                                                                         CKR5 MACMU
                                                                                               RESULT 13
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2 TTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATGCTACTGG 61
                                                                                                                                                            PEGNI; PRO0001; Tul.; 1.
PRINTS; PR00137; GPCRHODOPSN.
PROSITE; PR00237; G-PROTEIN_RECEP_FL_1; 1.
PROSITE; PS50362; G-PROTEIN_RECEP_FL_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCRCR OKMONOCYTE CHAMOALTIACTANT protein 1 receptor) (MCP-1-R) (CCR2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58B96C85909FACB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                   3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 GGAATCCTAAAACTCTGCTTCGGTGTCGAAAT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 AA.
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CYTOPLASMIC (F
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or send an email to license@lisb-sib.ch).
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                                                                                       EMBL; AF005660; AAB62554.1; -.
EMBL; AF005661; AAB62555.1; -.
EMBL; AF005662; AAB62556.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
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                             U77672; AAC51109.1; -. U73739; AAC51158.1; -. U96762; AAC34132.1; -.
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149.00
100.00%
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90.858
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NCBI_TaxID=9544;
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352 AA;
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MOD_RES
MOD_RES
MOD_RES
CARBOHYD
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Homo sapiens (Human).
                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                           Coughlin S.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region.
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                                                                                   AIDS Res. Bum. Retroviruses 17:981-986(2001).
-1- FUNCTION: RECEPTOR FOR THE MCP-1, MCP-3 AND MCP-4 CHEMOKINES.
TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS
                                                                                                                                                       -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A AND B (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00237; GECRRHODOPSN.
PROSITE; P800237; G-PROTEIN_RECEP_F1_1; 1.
PROSITE; P850062; G-PROTEIN_RECEP_F1_2; 1.
PROSITE; P850062; G-PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
                                   Margulies B.J., Hauer D.A., Clements J.E.; ^{\prime}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Matches:
Conservative:
Mismatches:
Indels:
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
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26
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360 AA;
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Best Local Similarity:
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P41597;
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SEQUENCE
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ID CKR2_HI
AC P41597
DT 01-NOV
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   SOLUTION OF THE STANDARD DESCRIPTION OF THE STANDARD DESCR
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MEDLINE-20501139; PubMed-11046064;
Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,
Chakravarty L., Kolatukudy P.,
"Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that
has tyrosine sulfation in a conserved extracellular N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE-97150864; PubMed-8995400; Wong L.-M., Myers S.J., Tsou C.-L., Gosling J., Arai H., Charo I.F.; Organization and differential expression of the human monocyte chemocatractant protein 1 receptor gene. Evidence for the role of the carboxyl-terminal tail in receptor trafficking."; J. Biol. Chem. 272:1038-1045(1997).
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-!- FUNCTION: Receptor for the WCP-1, WCP-3 and MCP-4 chemokines.
-!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
Transduces a signal by increasing the intracellular calcium ions level. Alternative coreceptor with CD4 for HIV-1 infection.
-!- SUBCELULUAR LOCATION: Infegral membrane protein.
-!- ALTERNATIVE PRODUCES: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *Molecular cloning and functional expression of two monocyte chemoattractant protein I receptors reveals alternative splicing of the carboxyl-terminal tails.";
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR2)
(Monocyte chemoattractant protein 1 receptor) (MCP-1-R) (CCR2)
CCR2 OR CMKBR2.
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                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McComble W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K., Giodi L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D., Chen C.N., Frans C., Fitzgerald M., See L.H., Tang M., Porcel B.M., Dragan Y., Glacalone J., Pae A., Powell B., Watanabe M., Dogett N., Garcia D., Sagripanti J.L.; Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-94195821; PubMed-8146186;
Charo I.F., Myers S.J., Herman A., Franci C., Connolly A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.; "CDNA cloning and functional expression of a human monocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chemoattractant protein 1 receptor.";
Biochem. Biophys. Res. Commun. 202:1156-1162(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756(1994).
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EMBL; U03905; AAA19120.1; -.
EMBL; D29984; BAA06253.1; -.
EMBL; U80924; AAC51637.1; -.
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SLEHIALGCRIARLOKPYCGGPGYRPGKNYKYTYGGLLDGR
GKGKSIGRAPEASLQDKEGA -> RYLSVFFRKHITKRFCK
QCPVFKRETVDGYTSINTPSTGEQEVSAGL (IN
                                   InterPro; IPR000276; GPCR_Rhodpsn.
Fram; PF00001; 7fm_1; 1.
PR1NTS; PR00021; 7fm_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
G_PROTIE; PS50562; G_PROTEIN_RECEP_F1_2; 1.
Alternative spliting. Transmembrane; Glycoprotein; Sulfation; Alternative spliting.
DOMAIN

1 42 EXTRACELINIAR PORMENTATIVE.
                                                                                                                                                                                                                                                    7 (POTENTIAL).
CYTOPLEASHIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
SULFATION.
                                                                                                                                  1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
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EXTRACELLUIAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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F865E0D39E74CF0F CRC64;
                                                                                                                                                                         3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                   374 AA; 41914 MW;
EMBL; U80924; AAC51636.1; -. EMBL; U95626; AAB57791.1; -. EMBL; U95626; AAB57792.1; -. Genew; HGNC:1603; CCR2.
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134.00
100.00%
96.30%
81.71%
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2222266
332868
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Query Match:
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Search completed: June 3, 2003, 18:46:03 Job time : 3.52995 secs

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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 12-Jul-1996 #text_change 20-Jun-2000
C; Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000
C; Accession: A43113; S71808, A58834; A58832; G02653, A58833
E; Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996
A; Title: Molecular cloning and functional expression of a new human CC-chemokine rece A; Reference number: A43113; MUID:96241590; PMID:8639488
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A; Cross-references: GB:X99393; NID:g1524062; PIDN:CAA67767.1; PID:g1524063
A; Orce: this frameshift mutation results in a non-functional receptor but confers a can amy have had a selective advantage by conferring resistance to Yersinia plague inf R; Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.
J. Leukoc. Biol. 60, 147-122, 1996
A;Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine A;Reference number: A58832; MUID:96295970; PMID:8699119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-352 <SAMI>
A; Cross-references: GB:X91492; NID:91262810; PIDN:CAA62796.1; PID:91262811
R; Samson, M.; Libert, F; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Sarag
M.; Imal, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.;
Nature 382, 722-725, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant allele
A;Reference number: S71808; MUID:96345670; PMID:8751444
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A;Residues: 182-206;207-230 <SAM2>
A;Accession: A58834
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A; Accession: A58832
A; Molecule type: mRNA
A; Residues: 1-352 <COM1>
A; Molecule type: DNA
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-Q-/cgn2_1/USPTQ_spool/USO9938703/runat_03062003_161407_22855/app_query.fasta_1.1870
-Q-/cgn2_1/USPTQ_spool/USO9938703/runat_03062003_161407_22855/app_query.fasta_1.1870
-DB-PIR_3 - CFWPT-fastan - SOFFIX=rpr - MINMARCH+0.1 - LOOPEL_0 - LOOPEZT=45
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 - TRANS=human40.cdi -LIST=45
-DCGALIGN=200 -THR_SCORE=pct - THR_MATRIX=100 -THR_MIN=0 -ALIGN=15 -MODE=LCCAL
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOOT=-30 -THREADS=1 -NGAROP==10 -NGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                 OM nucleic - protein search, using frame_plus_n2p model
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A Map position: 3p21-3p21
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Seywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane #status predicted <TML>
F; 44-68/Domain: transmembrane #status predicted <TMA>
F; 19-99/Domain: transmembrane #status predicted <TMA>
F; 115-136/Domain: transmembrane #status predicted <TMA>
F; 208-226/Domain: transmembrane #status predicted <TMA>
F; 208-226/Domain: transmembrane #status predicted <TMA>
F; 208-226/Domain: transmembrane #status predicted <TMA>
F; 209-20-309/Domain: transmembrane #status predicted <TMA>
F; 209-309/Domain: transmembrane #status predicted <TMA>
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C; Date: 16-Feb-196 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999
C; Date: 16-Feb-196 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999
C; Accession: 138450
R; Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. 0.S.A. 91, 2752-2756, 1994
A; Title: Molecular cloning and functional expression of two monocyte chemoattractant
A; Reference number: A53477; MUID:94195821; PMID:8146186
A;Cross-references: DDBJ:D29984; NID:9531246; PIDN:BAA06253.1; PID:9531247
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant A;Reference number: A53477; MUID:94195821; PMID:8146186
A;Status: preliminary
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-360 CRESS
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A;Molecule type: mRNA
A;Residues: 1-374 <RES>
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Description: G protein-coupled receptor for chemokines MIP-lalpha, MIP-labeta and RANTE A Note: probably acts to control granulocyte proliferation and differentiation c'superfamily: vertebrate rhodopal control granulocyte proliferation and differentiation c'superfamily: vertebrate rhodopal receptor; glycoprotein; phosphoprotein; transmembrane firstus predicted <TML>
F;32-56/Domain: transmembrane firstus predicted <TML>
F;103-114/Domain: transmembrane firstus predicted <TML>
F;103-124/Domain: transmembrane firstus predicted <TML>
F;103-125/Domain: transmembrane firstus predicted <TML>
F;26-257/Domain: transmembrane firstus predicted <TML>
F;26-257/Domain: transmembrane firstus predicted <TMC>
F;26-257/Domain: transmembrane firstus predicted <TMC>
F;26-257/Domain: transmembrane firstus predicted <TMC>
F;26-269,101-178/Disulfide bonds: firstus predicted <TMC>
F;26-269,101-178/Disulfide bonds: firstus predicted <TMC>
F;26-269,101-178/Disulfide bonds: firstus predicted <TMC>
F;346,337,342/Banding site: phosphate (TMT) (covalent) firstus predicted F;346,343/Banding site: phosphate (TMT) (covalent) firstus predicted
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Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A;Title: cDNA cloning and functional expression of a human monocyte chemoattractant prot A;Reference number: JC2443; MUID:94324942; PMID:8048929
A;Accession: JC2443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
Lstol. C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
A;Title: Molecular cloning and functional characterization of a novel human CC chemokine
A;Reference number: A58833; MUID:96291862; PMID:8663314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Cross-references: GB:U54994; NID:g1457945; PIDN:AACS0598.1; PID:g1457946
C;Comment: This is a receptor for chemokines MIP-lalpha (see PIR:A30574), MIP-lbeta (see
C;Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (
                  A;Cross-references: GB:U57840; NID:q1502408; PIDN:AAB17071.1; PID:q1502409
A;Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 TTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTCG 61
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C;Date: 21-Feb-1995 *sequence_revision 05-Apr-1995 *text_change 20-Jun-2000
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A;Gene: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CKR5; ChemR13
A;Cross-references: GDB:1230510; OMIM:601373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
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                                                                                                                                                     submitted to the EMBL Data Library, May 1996
                                                                                                                                                                                                                                                                           A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-89,'L',91-352 <COM2>
A;Cross-references: EMBL:U57840
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                                                                                                                                                                                          A; Reference number: H01541
A; Accession: G02653
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C; Function:
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A; Residues: 1-360 <YAM>
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A; Residues: 1-352 <RAP>
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A) Map position: 3p21-3p21
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane #status predicted <TML>
F; 71-91/Domain: transmembrane #status predicted <TML>
F; 71-91/Domain: transmembrane #status predicted <TMS>
F; 108-129/Domain: transmembrane #status predicted <TMS>
F; 205-223/Domain: transmembrane #status predicted <TMS>
F; 205-223/Domain: transmembrane #status predicted <TMS>
F; 205-223/Domain: transmembrane #status predicted <TMS>
F; 244-273,106-183/Disulfide bonds: #status predicted <TMS>
F; 244-273,106-183/Disulfide bonds: #status predicted
F; 345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicte
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N;Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C;Accession: A45177; L55671
R;Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk; R.; Schall, T.J.
Cell 72, 415, 425, 1993
A;Title: Molecular cloning, functional expression, and signaling characteristics of a A;Reference number: A45177; MUID:93161416; PMID:7679328
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A;11tle: Structure and functional expression of the human macrophage inflammatory 1 a A;Reference number: 155671; MUID:93240122; PMID:7683036
A;Accession: 155671
A;Title: Cloning and functional expression of a human eosinophil CC chemokine recepto A;Reference number: A57237; MUID:95348056; PMID:7622448
A;Accession: A57237
A;Status: nucleic acid sequence not shown
                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-106, NY, 108-275, 'S', 277-280, 'R', 282-355 <COM>
A; Cross-references: GB:U28694; NID:g1199579; PIDN:AAC50469.1; PID:g1199580
A; Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC504
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A;Experimental source: HL60 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:124876)
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Indels:
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A;Molecule type: mRNA
A;Residues: 1-355 <RES>
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Matches:
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A;Cross-references: GDB:138446; OMIM:601159
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A,Cross-references: GDB:579624; OMIM:601268
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A; Residues: 1-355 <NEO>
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Best Local Similarity:
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R; Gao, J.L.; Murphy, P.M.
B; Cao, J.L.; Murphy, P.M.
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C;Species: Homo saptes (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000
C;Accesion: G02436; A57237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIP-1 alpha receptor like-2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998
                  F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted F;32-277,113-190/Disulfide bonds: #status predicted
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C;Superfamily: vertebrate rhodopsin
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A.Molecule type: DNA
A.Residues: 1-355 <PON>
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74.39%
                                                                                                                                                      5.48e-11
134.00
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A,Cross-references: GDB:677463
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane #status predicted <TML>
F;40-65/Domain: transmembrane #status predicted <TML>
F;151-115/Domain: transmembrane #status predicted <TMA>
F;151-115/Domain: transmembrane #status predicted <TMA>
F;208-226/Domain: transmembrane #status predicted <TMA>
F;291-308/Domain: cransmembrane #status predicted <TMA>
F;291-308/Domain: status predicted <TMA>
F;291-308/Domain: status predicted <TMA>
F;291-308/Domain: status predicted <TMA>
F;291-308/Domain: status predicted <TMA>
F;391-Mainding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.
J. Biol. Chem. 270, 19495-19500, 1995
A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor A; Peference number. A57160; MUID:95370289; PMID:7642634
A;Rocession: A57160
A;Status; preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-360 cPOWA
A;Cross-references: GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452
A;Genetics:
A;G
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C;Accession: 158186
R;Harrison, J.K.; Barber, C.M.; Lynch, K.R.
Neurosoi. Lett. 169, 85-89, 1994
A;Title: cDNA cloning of a Grordein-coupled receptor expressed in rat spinal A;Reference number: 158186; MUID:94323113; PMID:8047298
A;Accession: 158186
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C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor
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A;Molecule type: mRNA
A;Residues: 1-354 <RES>
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       C; Superfamily: vertebrate rhodopsin
C; Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; t; 36-60/Domain: transmembrane #status predicted <TML>
F; 37-91/Domain: transmembrane #status predicted <TML>
F; 31-91/Domain: transmembrane #status predicted <TML>
F; 31-31/Domain: transmembrane #status predicted <TML>
F; 340-23/Domain: transmembrane #status predicted <TML>
F; 240-23/Domain: transmembrane #status predicted <TML>
F; 240-264/Domain: transmembrane #status predicted <TML>
F; 240-205/Domain: transmembrane #status predicted <TML>
F; 240-305/Domain: transmembrane #status predicted <TML>
F; Aniding site: carbohydrate (Asn) (covalent) #status predicted
F; 345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
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201 LeuLysLeuAsnLeuLeuGlyLeuIleLeuProLeuLeuValMetileIleCysTyrAla 220
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C.Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C.Accession: A57160
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: presidues: 1-555 CRBS
A;Status: DBBJ-UZ8404; NID:GBBJ547; PIDN:AAA89153.1; PID:GBBJ548
C;Superfamily: vertebrate rhodopsin
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A; Molecule type: mRNA
A; Residues: 1-355 <RAP>
A; Residues: 1-355 <RAP>
A; Cross-references: GB-102050; NID:9665580; PIDN:AAA91783.1; PID:9665581
A; Experimental source: peripheral blood mononuclear cell
C; Comment: This protein is a cell-surface receptor which recognizes extracellular sig
C; Comment: This protein is a key regulator of many immune and homeostatic responses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Gene: cc ckr-4
Cs.Superianlly: vertebrate rhodopsin
C; Superianlly: phosphoprotein; receptor; thymus
C; Keywords: glycoprotein; phosphoprotein; receptor; thymus
C; Keywords: glycoprotein; phosphoprotein; covalent) (by casein Kinase II) #status p
E; 2,183,194/Binding site: phosphate (Ser) (covalent) (by protein kinase I) #status predicte
E; 145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicte
F; 321/Binding site: phosphate (In) (covalent) (by protein kinase C) #status predicte
                                                                                                                                                                                                                                                                                                                                 C.Accession: JC4587
R.HOGGWERÍA. J. J. Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Blochem. Biophys. Res. Commun. 218, 337-343, 1996
A; Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines
A; Reference number: JC4587; MuID:96136324; PMID:8573157
A; Molecule type: MRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene V28 is closely related t
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2 ITAAAGATAGICAICTIGGGGCIGGICCIGCCGCIGCITGICAIGGICAICTGCTACICG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X90862; NID:q1167851; PIDN:CAA62372.1; PID:q1167852
A;Experimental source: thymus
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C.Specias: Homo sapiens (man)
C.Specias: Homo sapiens (man)
C.Specias: LoNov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
                                                                                                                                                                                                                                                       chemokine (C-C) receptor 4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
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C;Superfamily: vertebrate rhodopsin
C;Reywords: G protein-coupled receptor; lymphokine; transmembrane protein
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C; Accession: JC4304
R; Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, Gene 163, 295-299, 1995
A; Title: The orphan G-protein-coupled receptor-encoding gene V28 is cl A; Reference number: JC4304; MUID:96011651; PMID:7590284
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R;Gao, J.L.; Murphy, P.M.
Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemoki A;Reference number: I49339; MUID:95340546; PMID:7542241
A;Accession: I49340
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                                                                                                                                                                                                                                                                                                    G protein-coupled receptor El - equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Date: 10-Apr-1996 #text_change 13-Aug-1999
C;Dates: 10-Apr-1996 #text_change 13-Aug-1999
C;Accession: S55594
B;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2
A;Reference number: S55594; MuID:95302501; PMID:7783207
A;Accession: S55594
A;Steus: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-383 <TEL>
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
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A;Cross-references: EMBL:U28405; NID:g881549; PIDN:AAA89154.1; PID:g881550
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C;Superfamily: vertebrate rhodopsin
C;Reywords: G protein-coupled receptor
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       US-09-938-703-3_COPY_792_885 (1-94) x I58186 (1-354)
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A; Residues: 1-378 <SCH>
A; Residues: 1-378 <SCH>
A; Cross-references: GB:L31581; NID:g468319; PIDN:AAA74231.1; PID:g468320
R; Burgstahler, R.; Kempkes, B.; Staeube, K.; Lipp, M.
submitted to the EMBL Data Library, February 1995
A; Description: The expression of the chemokine receptor BLR2/EBI1 is specifically tra
A; Reference number: S52443
A;Title: Cloning of human and mouse BBII, a lymphoid-specific G-protein-coupled recep
A;Reference number: A55735; MUID:95154835; PMID:7851893
A;Accession: B55735
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Job time : 4.30469 secs
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C;Superfamily: vertebrate rhodopsin
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A; Molecule type: DNA
A; Residues: 21-378 <BUR>
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MyAlternate names: Burkht's lymphoma receptor 2; Epstein-Barr virus induced protein 1
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
C;Accession: B55735; S22443
R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B. Genomics 23, 643-650, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A;Title: Epstein Barr virus-induced genes: first lymphocyte-specific G protein-coupled
A;Title: Epstein mumber: A45680; MUID:93188173; PMID:8383238
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C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C;Accession: A45680
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A;Nofe: sequence extracted from NCBI backbone (NCBIN:127094, NCBIP:127095)
C; Superfamily: vertebrate rhodopsin
C; Reywords: G protein-coupled receptor; transmembrane protein
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              F;35-57/Domain: transmembrane #status predicted <TMl>+ f6-88/Domain: transmembrane #status predicted <TM2-F;104-125/Domain: transmembrane #status predicted <TM3-F;146-165/Domain: transmembrane #status predicted <TM3-F;197-211/Domain: transmembrane #status predicted <TM3-F;230-245/Domain: transmembrane #status predicted <TM5-F;230-245/Domain: transmembrane #status predicted <TM5-F;230-245/Domain: transmembrane #status predicted <TM6-F;230-245/Domain: transmembrane #status predicted <TM6-F;230-245/Domain: transmembrane #status predicted <TM6-F;240-246/Domain: transmembrane #status predicted <TM6-F;240-246/Domain: transmembrane #status predicted <TM6-F;240-246/Domain: transmembrane #status predicted <TM6-F;240-246/Domain: transmembrane #status predicted <TM7-F;240-246/Domain: transmembrane #status predicted <TM7-F;240-246/Domai
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A, Molecule type: nucleic acid
A, Residues: 1-378 <BIR>
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1122
1 MDYQVSSPIYDINYYTSEPC......AACHGHLLLGNPKNSASVSK 215
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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			Description	03 homo sapien			71 pan troglod	c0 hylobates m	99 gorilla gor	50 pan troglod	c8 colobus pol	c6 trachypithe	a3 hylobates a	62 pygathrix a	14 colobus gue	c7 nasalis lar	c3 miopithecus	70 pan troglod	49 cercocebus
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               Hahn B.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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"HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
EMBL, APOLIS39; AAB65739.1; ...
InterPro; IPR000276; GPCR_Rhodpsn.
                 Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G.,
                                                      and CCR5 polymorphism.";
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                                                                                                                                                                                                                                                                          84.2%; Score 945; DB 6; Length 35
98.4%; Pred. No. 2.9e-80;
tive 2; Mismatches 1; Indels
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40466 MW; 3FFFAC7ABAE1D4FB CRC64;
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352 AA; 40598 MW; 39688FA7004C952F CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                           PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                               "HIV-1 subtypes, co-receptor usage, and AIDS Res. Hum. Retroviruses 0:0-0(1997) RMBL, AF011541, AAB65741.1; -. InterPro; IRR000276; GPCR_Rhodpsn. Pfam; PF00001; 7tm_1; 1.
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Best Local Similarity 97.8
Matches 180; Conservative
                                                                                                                                                                                                                                                                                                 Local Similarity ...
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352 AA;
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STRAIN-CHCCR5-142A;
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SEQUENCE FROM N.A.
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181 HFPY 184
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                                   LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                    Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Zhang Y., Ryder O.A., Zhang Y.;
*Sequence comparison of the CCR5 gene in primates and primate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

84.4%; Score 947; DB 6; Length 352;
Best Local Similarity 98.4%; Pred. No. 1.9e-80;
Matches 181; Conservative 2; Mismatches 1; Indels
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SEQUENCE 352 AA; 40508 MW; F4F64B3AD5AF658A CRC64;
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Last annotation update)
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                               HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215
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InterPro; IPR000276; GPCR_Rhodpsn.
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HFPY 184
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SEQUENCE FROM N.A.
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01-DEC-2001 (
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01-MAR-2002
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                                                                                                            MEDIINE-99210133; PubMed-10195758; Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T., Lal R.B.; "Species-specific changes in the CCR5 gene from African and Asian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
NCBI_TaxID-9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.C., Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.; Mutations in CCRS-coding sequences are not associated with SIV carrier status in African nonhuman primates."; AIDS Res. Hum. Retroviruses 15:931-939(1999).
Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ; DB 6; ... 1.1e-79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 352;
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Mueller-Trutwin M.C., Barre-Sinoussi F., Fomsgaard A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AR045214; AAD44007.1; -
InterPro: IPR000276; GPCR_Rhodpsn.
Pfan; PF00017; TPR0017; TPR0017; TPR017.1; -
PR00171; PR001737; GPCRENDODSN.
                                                                                                                                                                                                                                                                                                                                                                                                    352 AA; 40529 MW; 1BE68C68FE2E7AD0 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last annotation update)
CC chemokine receptor type 5.
CCR5.
                                                                                                                                                                                   nonhuman primates.;
AIDS Res. Hun. Retroviriuses 15:479-483(1999).
EMBL), A1D291; A2D02660.1;
INTERPO. IPR000276; GPCR_Rhodpsn.
Pfam: PR00001; 7tm_1: 1.
PRIMIES: PR000237; GPCRRHODOPSN.
PRIMIES: PR000237; G_PROTEIN_RECEP_FI_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_FI_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 939; DB Pred. No. 1.1e-3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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97.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 179; Conservative
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181 HFPY 184
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                                                                    SEQUENCE FROM N.A.
                           NCBI_TaxID=9593;
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  Mammalia;
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Best Local S
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Q9TV50;
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Q9TV50
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                                                                                                                                              1 #DYQVSSPTYDIDYYTSGPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILLINCKR 60
                        LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTWCQLLTGLYFIGFFSGIFFII 120
                                                 LITIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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Gorilla gorilla (gorilla).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hylobates moloch (silvery gibbon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
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Zhang Y., Ryder O.A., Zhang Y.,
Sequence comparison of the CCR5 gene in primates and primate phylogeny.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.8%; Score 940; DB 6; Length 352; 97.8%; Pred. No. 8.6e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AR177899; AAKA3382.1; -1.
EMBL, AR177899; AAKA3382.1; -2.
Interop.: IPRO00276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CC Chemokine receptor 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                   352 AA
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HFPY 184
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SEQUENCE
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Q9XS99
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SEQUENCE FROM N.A.
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                                                                                                                              Trachypithecus.
NCBI_TaxID=66063;
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                                                                                                                                                                                           phylogeny.";
Submitted (A)
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                             095NC6
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                                                                                         1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                           Gaps
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                                     Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 938; DB 6; Length 35 Pred. No. 1.3e-79; 6; Mismatches 1; Indels
                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         phylogeny.",
Submitted (Aug.1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ART77881; ARK43364.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
PROSITE; PS00237; G.PROTEIN RECEP.F1_1; UNKNOWN_1.
PROSITE; PS00237; G.PROTEIN RECEP.F1_2; 1.
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                  40481 MW; 2578A0F2C07A4A65 CRC64;
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Last annotation update)
                                     Score 938; DB 6; L4
Pred. No. 1.3e-79;
5; Mismatches 1;
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PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                Created)
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96.2%;
                                      83.6%;
96.7%;
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Matches 177; Conservative
                                      Query Match 83.6
Best Local Similarity 96.7
Matches 178; Conservative
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HFPY 184
                   352 AA;
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          Receptor.
SEQUENCE
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 PROSITE;
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Q95NCB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIATURE-20317031; PubMed-10747879; Gonzalez E., Feuillet P.M., Mummidi S., Banshad M., Ahuja S.S., Gonzalez E., Feuillet P.M., Mummidi S., Banshad M., Ahuja S.S., Gonzalez E., Murthy K.K., Haro L., Dolan M.J., Allan J.S., Ahuja S.K.; "Evolution of human and non-human primate CC chemokine receptor 5 gene and mRNA. Potential roles for haplotype and mRNA diversity, differential haplotype-specific transcriptional activity, and altered transcription factor binding to polymorphic nucleotides in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
                                                                                                                                                                 Trachypithecus johnii (hooded leaf monkey).
Bukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae, Colobinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hylobates agilis unko.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (Aug-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF177883; AAK43366.1; ...
InterPro; IPR000276; GPCR_Rhodpsn.
PR00001; 7tm_1; 1.
PROSITE; PS00237; G PROTEIN RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor.
SEQUENCE 352 AA; 40462 MW; 52824E0322559F7F CRC64;
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01-OCT-2000 (TIEMBLIEL. 15, Last sequence update)
01-UDN-2001 (TIEMBLIEL. 17, Last annotation update)
CC_chemokine receptor 5.
                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.6%; Score 938; DB 6;
96.2%; Pred. No. 1.3e-79;
tive 6; Mismatches 1
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                                                 Created)
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PRT;
                                            01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 96.29
Matches 177; Conservative
                                                                                                                     C-C chemokine receptor 5.
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PRELIMINARY;
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61 LKSMTDIYLLNLAISDLFFILTVPFWAHYAAAQWDFGNTWCQLLTGLYFIGFFSGIFFII 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Colobus guereza (Black-and-white colobus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
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Spearman P.W., Mouru D.N., Graham B.S.;
Spearman P.W., Mouru D.N., Graham B.S.;
"Differential Utilization of CCR5 Molecules from Three East African Simian Species by the HIV-1 Envelope Glycoprotein.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
BEMBL, AF141639, AND32684.1;
InterPro; IPR000276; GCR2.Rhodpsn.
PROMPS: PR00027; GPROTENL RECEP_F1.1; UNKNOWN_1.
PROSTIE; PS00237; GPROTENL RECEP_F1.2; 1.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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Best Local Similarity 95.7%; Pred. No. 3.1e-79;
Msmacches 2;
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                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, C) 01-NOV-1999 (TrEMBLrel. 12, Lk 01-DEC-2001 (TrEMBLrel. 19, Lk CC chemokine receptor 5.
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HFPY 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Colobus.
NCBL_TaxID=33548;
                                                                                                                                         HFPY 184
                                                                                                                                                                                             181 HFPY 184
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01-MAR-2002
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                Q9XT14;
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                                                                                                                                                                                                                                                                             RESULT 12
Q9XT14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pygathrix avunculus (Tonkin snub-nosed monkey), and Pygathrix roxellana (golden snub-nosed monkey).
Bukaryota: Metazoa; Chordata; Caraitata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                                                                                                                                                                                                                                                                                                                                                    1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILLLINCKR
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                                                                                                                                                                                                                                                                                                          Score 935; DB 6; Length 352;
Pred. No. 2.5e-79;
pathogenesis of HIV-1 and simian immunodeficiency virus."; J. Biol. Chem. 275:18846-18951(2000).

EMBL. ARZF2551; ARMF9981.1; -.
InterPro; IPR000276; GFCR_Rhodpsn.

Pfam; PF00001; 7tm_1; 1.
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95.7%; Pred. No. 2.5e-79;
ive 7; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                      SEQUENCE 352 AA; 40293 MW; BAF8279ABBAB5309 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                                            PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352 AA.
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                                                                                                                                                                                                                                                                                                            83.3%;
96.7%;
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Best Local Similarity 95.7
Matches 176; Conservative
                                                                                                                                                                                                                                                                                                               Query Match 83.3
Best Local Similarity 96.7
Matches 178; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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HFPY 184
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                                                                                                                                                                                                                                        Receptor.
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61 IKSMTDIYLLNIAISDILELLITVPFWAHYAAAQWDFGNTWCQLLIGLXFIGFFSGIFFII 120
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                                                                     LKSMTDIYLLINLAISDLLFLLTVPFWAHYAAAQWDFGNTMCRLLTGLYFIGFFSGIFFII 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
NCBL_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ho D.D.;
"HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
AIDS Res. Hum. Retroviruses 0:0-0(1997).
EMBL, AP011538; AAB65738.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.2%; Score 933; DB 6; Length 352; 96.2%; Pred. No. 3.8e-79; Live 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352 352
352 AA; 40523 MW; 4513DB983A28ACB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                 352 A.A.
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                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                               05,
19,
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177; Conservative
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01-JAN-1998 (TrEMBLrel. 05
01-DEC-2001 (TrEMBLrel. 15
CCR5 receptor (Fragment).
                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
STRAIN=MACCR5-140A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          completed: June
ne : 44.5732 secs
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HFPY 184
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Matches
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecimae; Miopithecus.
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Zhang Y., Ryder O.A., Zhang Y.;

Zhang Y., Ryder O.A., Zhang Y.;

Sequence comparison of the CCR5 gene in primates and primate phylogeny.

Submitted (ANG-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, ARIJOSE, AAR43186.1;

InterPro; IPR0001276; GPCR_Rhodpsn.

Pfam: PRO0011, 7tm.1, 1.

PROSITE; PS000137; G_POTEIN_RECEP_F1.1; UNKNOWN_1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1.2; 1.
                                                      SEQUENCE FROM N.A.
Zhang Y., Ryder O.A., Zhang Y.;
"Sequence comparison of the CCR5 gene in primates and primate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.2%; Score 934; DB 6; Length 352; 96.2%; Pred. No. 3.1e-79; tive 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                             Length 352;
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                                                                                                                                phylogeny.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
BMEL; AFI77882; AAK43365.1;
INTER-PTO; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PROSTTE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSTIE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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SEQUENCE 352 AA; 40546 MW; 6464152F3E566AE5 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Pred. No. 3.1e-79;
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          WCBI_TaxID-43780;
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 3, 2003, 19:18:46; Search time 12.2358 Seconds (without alignments) 728.798 Million cell updates/sec Run on:

US-09-938-703-6 1122 1 MDYQVSSPIYDINYYTSEPC......AACHGHLLLGNPRNSASVSK 215 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	P51681 homo sapien				_	•					-		P51682 mus musculu	O08556 rattus norv	P51683 mus musculu	O55193 rattus norv	P41597 homo sapien	018793 macaca mula	P32246 homo sapien	P51675 mus musculu	P56482 macaca mula		mns	P51678 mus musculu	_	~	_	56483		mus	mus m	P51685 homo sapien
El .	CKR5_HUMAN	CKR5 PONPY		CKR5_PYGBI	CKR5_PYGNE	CKR5_TRAFR	CKR5_TRAPH	CKR5_HYLLE	CKR5_MACMU		CKR5_CERTO	CKR5_CERAE	CKR5_MOUSE	CKR5_RAT	CKR2_MOUSE	CKR2_RAT	CKR2_HUMAN	CKR2_MACMU	CKR1_HUMAN	CKR1_MOUSE	CKR1_MACMU	CKR4_HUMAN	CKR4_MOUSE	CKR3_MOUSE	CKR3_RAT	CKR3_CAVPO	CKR3_HUMAN	CKR3_MACMU	CKR3_CERAE	CKRV_MOUSE		CKR8_HUMAN
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% Query Match	85.4	84.9	84.0	83.6	83.6	83.6	83.6	83.4	83.2	83.2	82.7	81.6	70.1	69.1	63.8	63.7	61.9	61.3	53,3	50.8	50.1	48.8		47.7	47.7	46.0	45.1	44.5	43.6	43.6	38.4	38.1
Score	958	952	942	938	938	938	938	936	933	933	928	916	786	775	715.5	714.5	694	689	598	570.5	562	547.5	546.5	535.5	535.5	516.5	506.5	499.5	489.5	489.5	431	427.5
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097665 macaca mula P35411 rattus norv Q92049 mus musculu Q9wut7 mus musculu P49238 homo sapien P51686 homo sapien P3248 homo sapien P4774 mus musculu Q62747 cercocebus P30991 macaca mula Q00590 homo sapien	
CKR8_WACMU C3X1_RAT C3X1_RAT C3X1_LWOUSE C3X1_HUWAN CKR9_HUWAN CKR7_HUWAN CKR7_HUWAN CKR7_WOUSE CCR4_CCRTC CCR4_HUWAN CCR4_HUWAN CCR4_HUWAN CCR4_HUWAN CCR4_HUWAN CCR4_HUWAN	
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ALIGNMENTS

RESULT 1

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires alloense agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell 96:667-676(1999).

-1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEYEL. MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERANTION OR DIFFERENTIATION. ACTS AS CO-RECEPTON WITH CD4 FOR PRIMARY NON-SYNCTIUM-INDICING STRAINS (NSI) (MACROPERAGE-TROPIC) OF HIV-1 VIRUS. IT PROMOTES ENV-MEDIATED FUSION OF THE VIRUS.
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                                                                                                             MEDILINE-98049523; Pubmed-9388201; Mummid1 S.K.; McDaniel B.L., Ahuja S.K.; McDaniel B.L., Ahuja S.K.; McDaniel B.L., Ahuja S.K.; McDaniel B.L., Ahuja S.K.; Multiple transcripts with 5'-end heterogeneity, dual promoter usage, and evidence for polymorphisms within the regulatory regions and noncoding exons.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99189752; PubMed-10089882; Patt R., Cayabyab M., Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M., Choe H.; Grard C., Sodroski J., Choe H.; "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLYCOSYLATION. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Paxton W.A.; "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
                                      thang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- TISSUB SPECIFICITY: FOUND IN PROMYELOCYTIC CELLS.
-i- PPM: SULRATION COMPILEDITES TO THE EFFICIENCY OF HIV-1 ENTRY.
-i- PPM: MODIFIED BY O-LINKED GLYCOSYLATION, BUT NOT BY N-LINKED
                                                             "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism."; AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
                                                                                                                                                                                                                                                                       CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
MEDLINE-96260017; PubMed-8649511;
Deng H., Liu R., Ellmeter W., Choe S., Unutmaz D., Burkhart M.,
di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,
Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
"Identification of a major co-receptor for primary isolates of
                                                                                                                                                                                                                                                                                                                                                                                                                    Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,
                                                                                                                                                                                                                       Magierowska M., Barre-Sinoussi F., Issafras H., Theodorou I.,
                                                                                                                                                                                                                                                 Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                            CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION. MEDLINE-96260018; PubMed=8649512;
                                                                                                                                                                                                            SEQUENCE FROM N.A., AND VARIANT ARG-178.
[6]
SEQUENCE FROM N.A., AND POLYMORPHISMS.
MEDLINE-98022612, PubMed-9359654;
MEDLINE-98022612, PubMed-9359654;
                                                                                                                                                                                  Biol. Chem. 272:30662-30671(1997).
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                                                                                                     SEQUENCE FROM N.A.
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
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/FTIG=VAR.003481.
A -> S (IN DBSNP:1800939).
/FTIG=VAR.011839.
R -> H (IN INCCR5-72A).
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EXTRACELLULAR (POTENTIAL).
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PRINTS; PR00237; GPCRRHODOPSN.
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AF031237; AAB94735.1;
AF052539; AAD18131.1;
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AF011536; AAB65736.1;
AAB65708.1;
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MIM; 60
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This SWISS-PROT entry is copyright. It is produced through a collaboration
SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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2; Mismatches
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                                                                                                                                                         EMBL; AF011540; AAB65740.1; -.
EMBL; U89797; AAC03717.1; -.
Interpro; IPR000276; GPCR_Rhodpsn.
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                                                                                                                 EMBL; AF005663; AAB62557.1; -.
                                                                                                                            EMBL; U94329; AAB58446.1; -.
EMBL; AF011542; AAB65742.1; -.
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98.9%;
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123
352 AA;
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CARBOHYD
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                                                                                                                                                   121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPL/SLVFIFGFVGNMLVILLINCKR 60
                                                     1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97426118; PubMed-9282822; Zacharova V., Zachar V., Goustin A.S.; *Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
                                                                                                                                                                                                                                                                     P56440; 002778;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
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MEDILINE-97268687; PubMed=9108095;
Bdinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Edinger A.L., Amedee M., Lu E.H., Clements J.E., Murphey-Corb M.,
Paiper S.C., Parmentier M., Broder C.C., Doms R.W.;
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
Pfiferential utilization of CCRS by macrophage and T cell tropic
sinian immunodeficiency virus strains.";
Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
                                                                                                                                                                                                                                                                                                                                     Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism."; AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
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            85.4%; Score 958; DB 1; Length 352;
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Zimmerman P.A., Buckler-White A., Alkhatib G.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                  Indels
                       Pred. No. 2.3e-53;
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SEQUENCE FROM N.A.
MEDLINE-98090115; PubMed-9430250;
MEDLINE-98090115; PubMed-9430250;
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                                     184; Conservative
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SULFATION (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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PROSITE; PS00237; GPROTELN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTELN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; 1.

DOMAIN 1 30 EXTRACELULAR (POTENTIAL).

TRANSHEM 31 58 I (POTENTIAL).
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CYTOPLASHIC (POTENTIAL).
BY SIMILARITY.
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
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6 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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4 (POTENTIAL).
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Score 952; DB 1; Leny
A No. 5.4e-53;
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121 LLTIDRYLAIVHAVFALKARIVTFGVVTSVIIWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                                                                                                                                                                                                                                                                                                                                                    Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
Pelper S.C., Parmentier M., Broder C.C., Doms R.W.;
"Differential utilization of CCR5 by macrophage and T cell tropic
simian immunodeficiency virus strains.";
Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
-I- FUNCTION: RECEPTOR NA C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANNES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
                                                                                                                                                                                                              tel. 36, Last sequence update)
tel. 40, Last annotation update)
receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN 1 30 EXTRACELUIAR (POTENTIAL).
TRANSMEM 31 58 1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBCELIULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                            Gorilla gorilla gorilla (Lowland gorilla).
Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IN THE CONTROL OF GRANDLOCYTIC LINEAGE PROLIFERATION OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
SULFATION (BY SIMILARITY).
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EXTRACELLULAR (POTENTIAL).
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InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                              PRT;
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                                                                                                                                                                                           15-JUL 1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
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352 AA;
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                                                                                                                                                                                         Zhang Y.-W., Ryder O.A., Zhang Y.-P.;

"Sequence evolution of the CCR5 chemokine receptor gene in primates.";

Mol. Biol. Evol. 16:1145-1154(1999).

-I-FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,

MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELIDIAR CALCIUM IONS LEYEL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
DIFFERENTIATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MDYQVSSPIYDINYXTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
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     30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5)
                                                                                                                                                                                                                                                                                                                                    -1- SUBCELLUIAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation. DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
                                                                                          Eukāryotā; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
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40527 MW; F4E2F47135AF658A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 947; DB 1;
Pred. No. 1.1e-52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF075446; AAD19858.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                              MEDLINE-99416438; PubMed-10486970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.48;
98.48;
                                                                           Pongo pygmaeus (Orangutan).
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Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00001; 7tm_1;
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14
15
352 AA;
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                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                               NCBI_TaxID=9600;
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EXTRACELLULAR (POTENTIAL).
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InterPro; IPR000276; GPCR_Rhodpsn.
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                                                                                                                                                                                                                                       40585 MW;
                                                                                                                                                                                                                                                                               83.68;
96.28;
                                                                                                                                                                                                                                                                                                      Best Local Similarity 96.2 Matches 177; Conservative
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198
235
250
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352
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352 AA;
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097882;
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SEQUENCE
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DOMAIN
                                                          PRANSMEM
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                                                                                                                                                                                                          121 ILTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                                                                                                                                                                                                                                      61 LKSMTDIYLLNLAISDLFFLLIVPFWAHYAAAQWDFGNTMCQLLIGLYFIGFFSGIFFII 120
                                                                                                       9
                                                                                                                            1 MDYQVSSPTYDIDYYTSEPCQKTNVKQIAARLEPPLYSLVFIFGFVGNMLVILLINCKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
"Sequence evolution of the CCR5 chemokine receptor gene in primates.";
"Sequence evolution of the CCR5 chemokine receptor gene in primates.";
MOI. BJOL. Evol. 16:1145-1154(1999).
-I- BTOM AND RAPPES AND SUBSEQUENTY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEYEL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Būkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
Pygathrix.
                                                                                                       1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last amortation update)
-c. chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5).
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Prints; PR000237; GPCRRHODDPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS500262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS500262; G_PROTEIN_RECEP_F1_2; 1.
G_protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN 1 30 EXTRACELLUIAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pygathrix biet1 (Black snub-nosed monkey) (Rhinopithecus bieti).
                                                               0;
                         Length 352;
                                                                 Indels
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
                           Score 942; DB 1;
Pred. No. 2.3e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352 AA.
                                                                   2; Mismatches
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SEQUENCE FROM N.A.
MEDLINE-99416438; PubMed=10486970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF075445; AAD19857.1; -
                                                                   Matches 180; Conservative
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58
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181 HFPY 184
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TRANSMEM
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                               Query Match
                                                Best Local
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDYQVSSPTYDIDYYTSEPCQKVNVKQIAARLLPPLYSLVFIEGFVGNILVVTILINCKR 60
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- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
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Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                           7 (POTENTIAL).
CYTOPLASHIC (POTENTIAL).
BY SIMILARITY.
SULFATION (BY SIMILARITY).
                                                                   6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 938; DB 1;
Pred. No. 4e-52;
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6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LKSMTDIYLLNLAISDLFFILITVPFWAHYAAAQWDFGNTWCQLLIGLYFIGFFSGIFFII 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MDYQVSSPIYDIDYYTSEPCQXVNVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trachypithecus phayrei (Phayre's leaf monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CRR-5) (CC-CKR-5) (CCR-5).
                                                                                                                                  EMEL; AF075442; AAD19854.1; ...
INTERFO; IPR000276; GPCR_Rhodpsn.
PRIMTS: PR00237; GPROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 938; DB 1; Length 352;
Pred. No. 4e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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SULFATION (BY SIMILARITY)
SULFATION (BY SIMILARITY)
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
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SULFATION (BY SIMILARITY)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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96.28;
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Matches 177; Conservative
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352
178
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181 HFPY 184
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"Sequence evolution of the CCR5 chemokine receptor gene in primates.",
Mol. Biol. Bvol. 16:1145-1154(1999).
-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSOUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
IN THE COMPROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
                                                                                                                                                                                                                                                                                                                                                                                                                  1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
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15-JUN-2002 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR-5)
       Pfam, Fruvo., ...
PRINTS, PRO0237, GPCRRHODOPSN.
PROSITE; PRO0237, G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
EXTRAGELULIAR (POTENTIAL).
EXTRAGELULIAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                Score 938; DB 1; Length 352;
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CYTOPLASHIC (POTENTIAL).
BY SIMILARITY.
SULFATION (BY SIMILARITY).
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EXTRACELLULAR (POTENTIAL).
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3 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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    Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                       40532 MW;
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96.2%;
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352 AA;
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HFPY 184
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                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                            SEQUENCE FROM N.A.

MEDLINE-99416438; PubMed-10486970;

Zhang Y.-P.;

Zhang Y.-P.;

Sequence evolution of the CCR5 chemokine receptor gene in primates.";

MOL. Biol. Evol. 16:1145-1154(1999).

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MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY

INCREASING THE INTERCELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE

IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
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PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.

EXTRACELLULAR (FOIENTIAL).

EXTRACELLULAR (FOIENTIAL).
                                                                                                                              SUBCELLURAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
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EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Interpro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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96.28;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDIINE-99416438; PubMed=10486970;
MEDIINE-99416438; PubMed=10486970;
"Sequence evolution of the CCR5 chemckine receptor gene in primates.";
Mol. Biol. Evol. 16:1145-1154(1999).
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MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
IN THE CONTROL.
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PRINTS; PR00237; GPROTEIN RECEP_F1_1; 1.

PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

EXTRACELLULAR (POTENTIAL).
                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CRR-5) (CC-CRF-5) (CCR-5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                     Hylobates leucogenys (White-cheeked gibbon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 352;
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Pred: No. 5.4e-52;
3; Mismatches 2; Indels
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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SULFATION (BY SIMILARITY)
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4F8E4F344CEB7C91 CRC64;
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SIMILARITY)
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CYTOPLASMIC (POTENTIAL).
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Interpro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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352 AA;
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nes 179; Conserv
                                                                                                                                                                                                                                               NCBI_TaxID=61853;
                                                                                                                                                CCR5 OR CMKBR5.
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EMBL; AP005660; AAB6254.1; -.
EMBL; AP005661; AAB6255.1; -.
EMBL; AP005661; AAB62555.1; -.
EMBL; AP005662; AAB62556.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
PFam; PP00001; 7tm_1; 1.
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15-JUL-1998 (Rel. 36, Last segu
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40507 MW;
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                                                                                                                              EMBL; U77672; AAC51109.1; -.
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HFPY 184
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CKR5_PAPHA
ID CKR5_PAPHA
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LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                           SPECIES-M.mulatta; STRAIN-Indian macaque;
MEDLINE-97213934; PubMed-9060623;
Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
Genetically divergent strains of simian immunodeficiency virus use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5).
                                                                                                                                                                                                                                                                                                                                                                                                  Macaca mulatta (Rhesus macaque),
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES-M.mulatta;
MEDLINE-21354176; PubMed=11461684;
Margulies B.J., Hauer D.A., Clements J.E.;
"Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                      Macaca nemestrina (Pig-tailed macaque).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-M.mulatta;
MEDLINE-97184592; PubMed-9032394;
Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
Newman W., Gerard N., Gerard C., Sodroski J.;
17:111zation of C.C chemokine receptor 5 by the envelope
17:111zation of C.C chemokine receptor 5 by the solvency
17:112ation of a pathogenic simlan immunodeficiency virus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIDS Res. Hum. Retroviruses 17:981-986(2001)
                                                                                                                                                                                                                                                                     352 AA.
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                                                                                                                                                                                                                                                                                                           (Rel. 35, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cercopithecinae; Macaca.
NCBI_TaxID=9544, 9541, 9545;
                                                                                                                                                                                                                                                                       STANDARD;
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01-NOV-1997 (Re.
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CKR5_MACMU
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between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCK5).
                                                                                                                                                                                                                                                                                                                                                                           finterPro; .....
Prim; PF00001; 7tm_1; 1.
PRINTS; PF00027; GPROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; Transmembrane; Glycoprotein; Sulfation.
EXTRACELLUIAR (POFENTIAL).
EXTRACELLUIAR (POFENTIAL).
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USULFATION (BY SIMILARITY).
N-LINKED (GLORAC. . .) (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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I -> M (IN REF
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CYTOPLASMIC (PC
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InterPro; IPR000276; GPCR_Rhodpsn.
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                              SPECIES-P. anubis.

Behton P.A., Timmans D.K., Shearer M.H., Lee D.R., Kennedy R.C.;

Behton P.A., Timmans D.K., Shearer M.H., Lee D.R., Kennedy R.C.;

Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BIRDS TO MIP-1-ALPHA,

MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY

INCREASING THE INTRACELLUTAR CALCIUM IONS LEFFEL. MAY PLAY A ROLE
                                                                                                                                                                                                                                                      SPECIES-P.hamadryas;
MEDLINE-9921013; PubMed-10195758;
Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;
"Species-specific changes in the CCR5 gene from African and Asian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sulfation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1 - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                     SPECIES-P. hamadryas;
MEDINE-97268687; PubMed-9108095;
Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Edinger A.L., Amedee A., Miller K., Clements J.E., Murphey-Corb M.,
Patron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
Petper S.C., Parmentier M., Broder C.C., Doms R.W.;
"Differential utilization of CRCF by macrophage and T cell tropic sintan immunodeficiency virus strains.";
Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                       IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIMES PRO00275; GPCR_Rhodpsn.

PRIMES: PR000237; GPCRRHODDPSN.

PROSITE; PS00237; GPCRRHODDPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                   AIDS Res. Hum. Retroviruses 15:479-483(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
             Papio hamadryas (Hamadryas baboon), and Papio anubis (Olive baboon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF005658; AAB62552.1; --
EMBL; AF105287; AAD20556.1; --
EMBL; AF105288; AAD20557.1; --
EMBL; AF105289; AAD20558.1; --
EMBL; AF105290; AAD20559.1; --
EMBL; AF105290; AAD20559.1; --
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68
89
102
1124
1141
1166
1198
235
235
3301
332
                                                                  Cercopithecinae; Papio.
NCBI_TaxID=9557, 9555;
                                                                                                                                                                                                                                                                                                         nonhuman primates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIFFERENTIATION
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                      1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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Virology 246:113-124(1998).
-!- FUNCTION: RECEPTOR FOR A C-C IYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
                                                                                                                                                                                                                                                                                                                                                  MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGRAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-ISOJATE 079, 085, 087, and 089;
MEDLINE-98121155; PubMed-9656999;
Chen Z., Gettle A., Ho D.D., Marx P.A.;
*Primary SIVsm isoJates use the CCR5 coreceptor from sooty mangabeys naturally infected in west Africa: a comparison of coreceptor usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CKR5_CERTO STANDARD; PRT; 352 AA.

062743; 062744; 062245; 062746;
15-DEC-1998 (Rel. 37, Created)
11-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5).

CCR5 OR CMKBR5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLUIAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini; Cercopithecidae,
                                                                                                                                LINKED (GLCNAC. . .) (POTENTIAL). 5E1504A9BA1FE8B2 CRC64;
                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                            Length 352;
                                                                                                                                                                                                               Score 933; DB 1; Length 35
Pred. No. 8.3e-52;
); Mismatches 2; Indels
BY SIMILARITY.
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
N-LINKED (GLCNAC. ..) (POI
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                                                                                                                                                                                                                                                                       5;
                                                                                                                                                            40489 MW;
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                                                                                                                                                                                                                 83.2%;
96.2%;
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14
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268
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15
268
352 AA;
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                                                                                                                                                                                                                                           Similarity
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                                                                                                                                      CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-JUL-1998 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CRR-5) (CCR-5) (CCR5).
CCR5 OR CMEBR5.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPERHOODEN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
EXTRACELLUIAR (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cercopithecus aethlops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                        BY STRILARITY.
SULFATION (BY SIMILARITY).
D -> E (IN ISOLATE 087).
Y -> G (IN ISOLATE 079).
W -> K (IN ISOLATE 079).
L -> V (IN ISOLATE 079).
V -> G (IN ISOLATE 079).
T -> I (IN ISOLATE 079).
T -> I (IN ISOLATE 079).
T -> I (IN ISOLATE 079).
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                                                                                                                                                                                                                             4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
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Pred. No. 1.7e-51;
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                                                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                             (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                 7 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40489 MW;
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95.7%;
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15
2
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25
100
107
134
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HFPY 184
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236
261
278
302
101
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P56493;
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CKR5_CERAE
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-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEWOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEYEL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
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EMBL; AB015944; BAA3128.1; -.

Interpro; IRRO0276; GPCR_Rhodpsn.

Pfan; PF00017; Tar.1; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation; Polymorphism.
                                                                                                                                                                                                                                                                                                                                            -- SUBCELLUIAR LOCATION: Integral membrane protein.
-- SIMILARIT: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
MEDLINE-98001387; PubMed-934322; Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.; Platt E.J., Kozak S.L., Kabat D.; Polymorphisms in the CCR5 genes of African green monkeys and mice implicate specific amino acids in infections by simian and human implicates pecific amino acids in infections by simian and human
                                                                                                                                                   Murayama Y., Matsunaga S., Inoue-Murayama M.;
"CDNA sequence of African green monkey CCR-5 chemokine receptor
gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 9.4e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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Best Local Similarity 95.1
Matches 175; Conservative
                                                                                     immunodeficiency viruses
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Submitted (JAN-1997) to the EMBL/Genbank/DbbJ databases.
-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCLUM IONS LEVEL.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H., Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.; Two distinct CCR5 domains can mediate coreceptor usage by human
                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning and functional expression of murine JE (monocyte chemoattractant protein 1) and murine macrophage inflammatory protein laippa receptors: evidence for two closely linked C-C chemokine receptors on chromosome 9.";
                                                                                                                                  ECERE_MOUSE STANDARD; PRT; 354 AA.
P51682; Q61867; P97405; O35313; P97308; O35891;
01-CCT-1996 (Rel. 34, Created)
15-JUL-1998 (Rel. 36, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (MIP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-C57BL/6, and NIH Swiss; TISSUE-Liver, Kidney, and Spleen; MEDLINE-98001387; PubMed=9343222; Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.; Polymorphisms in the CCRS genes of African green monkeys and mice implicate specific amino acids in infections by simian and human immunodeficiency Virusees."; J. Virol. 71:8642-8656(1997).
                                                                                                                                                                                                                                     Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A., "Cloning and characterization of a novel murine macrophage inflammatory protein-1 alpha receptor.";
J. Biol. Chem. 271:1445-14451(1996).
                                                                                                                                                                                                                                                                                                                                Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L., Charo I.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-C57BL/6 X CBA; TISSUE-Thymus;
MEDLINE-96278910; PubMed-8662890;
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STRAIN-129/SvJ; TISSUE-Spleen;
MEDLINE-96205938; PubMed-8631787;
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J. Virol. 71:6305-6314(1997).
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181 HFPY 184
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50362; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.

BXTRACELLULAR; (POTENTIAL).
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-1- TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CELL LINES,
BUT NOT IN NONHEMATOPOLETIC CELL LINES.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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1.1e-42;
18; Indels
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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(IN REF. 5).
(IN REF. 5).
(IN REF. 3).
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                                                                                                                                                                                  EMBL: X94151; CAA63867.1; -.
RMBL: U68565; AA37273.1; -.
RMBL: U83327; AAC53386.1; -.
EMBL: AF022990; AAC53389.1; -.
EMBL: AF019772; AAB71183.1; -.
EMBL: BRS (SR : BAA12024.1; -.
MGD: MGT.107182; CMkbr5.
InterPro; IPR000276; GPCR_Rhodpsn.
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Matches 149; Conservative
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                 IILLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Sprague-Dawley;

WEDLINE-Sprague-Dawley;

Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,

Deficer C.M., Pennell N.A., Streit W.J., Harrison J.K.;

Deficer c.M., Pennell N.A., Streit W.J., Harrison J.K.;

Deficer c.M., Pennell N.A., Streit W.J., Harrison J.K.;

J. Chemokine receptor expression in cultured gila and rat experimental allergic encephalomyelitis.";

J. Neuroimmunol. 86:1-12(1998).

I. Neuroimmunol. 86:1-12(1998).

I. POURTIN: RESEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,

MIP-1-BETA AND RAMES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Wistar; TISSUE-Brain;
MEDINITE-98334064; PubMed-96670989;
Spleiss O., Gourmala N., Bodeke H.W.G.M., Sauter A., Flebich B.L.,
Berger M., Gebicke-Haerter P.J.;
"Cloning of rat HYV-1-chemckine coreceptor CKR5 from microglia and
upregulation of its mRNA in ischemic and endotoxinemic rat brain.";
J. Neurosci. Res. 53:16-28(1998).
                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
03-MAY-2000 (Rel. 39, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CR-5) (MIP-1
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PRINTS; PR0027; GPREMEDOPSN.

PROSTIE; PS0033; G_PROTEIN_RECEP_F1_1; 1.

PROSTIE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein.

32 EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EMBL; U77350; AAC03243.1; --
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_l; 1.
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                                                                                                                                                                       CKR5_RAT
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CKR5_RAT
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TRANSMEM

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                                                                                                                                                      28
                                                                                                                                                                                                     59 KRLKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFF
                                                                                                                                                     1 MDYQVSSP--IYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINC
                                                                                                                               Gaps
                                                                 -LINKED (GLCNAC. ..) (POTENTIAL). 77EDB368AAC868D CRC64;
                                                                                                                               ;
                                                                                                       Length 354;
                                                                                                                              21; Indels
          6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
 (POTENTIAL).
                                                                                             Score 775; DB 1;
                                                                                                                  ; Pred. No. 5.5e-
18; Mismatches
                                                        BY SIMILARITY
N-LINKED (GLC)
 CYTOPLASMIC
                                                                                  41030 MW;
                                                                                                       69.1%;
78.2%;
                                                                                                                 Best Local Similaring
237
262
279
303
354
180
270
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                                                                                354 AA;
                      263
280
304
103
270
 DOMAIN
TRANSMEM
DOMAIN
TRANSMEM
                                                 DOMAIN
DISULFID
                                                                                                          Query Match
                                                                      CARBOHYD
                                                                                    SEQUENCE
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Search completed: June 3, 2003, 19:22:56 Job time: 13.2358 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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using sw model protein search, OM protein -

(without alignments) 875.891 Million cell updates/sec June 3, 2003, 19:20:46; Search time 23.5976 Seconds Run on:

US-09-938-703-6 1122 1 MDYQVSSPIYDINYYTSEPC......AACHGHLLLGNPKNSASVSK 215 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

283224 Total number of hits satisfying chosen parameters: 283224 seqs, 96134422 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 su

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	chemokine (C-C) re	chemokine (C-C) re	chemokine (C-C) re	chemokine (C-C) re	macrophage inflamm	chemokine (C-C) re	chemokine (C-C) re	MIP-1 alpha recept	chémokine (C-C) re	MIP-1 alpha recept	G protein-coupled	G protein-coupled	probable G protein	chemokine receptor	orphan G protein-c	lymphocyte-specifi	G protein-coupled	G protein-coupled	neuropeptide Y/pep	neuropeptide Y/pep	fusin (LESTRA) - c	angiotensin II rec	G protein-coupled	angiotensin II rec	angiotensin II rec	Н	angiotensin II rec	angiotensin II rec	angiotensin II rec
	Π	A43113	JC2443	I38450	A45177	149339	A57160	JC4587	149341	G02436	I49340	\$55594	JC5067	158186	JC5942	JC4304	B55735	A55735	A45680	A45747	S28787	G00048	151372	JC5068	JC1194	A42656	JC1104	I39418	JC2134	S15403
	DB	7	7	~	~	7	C3										• •		ď											7
	Query Match Length	352	360	374	355	355	360	360	359	355	356	383	355	354	344	355	378	378	378	352	353	352	359	369				359	359	359
dР	Query Match	85.4	61.9	61.9	53.3	51.1	48.8	48.7	47.7	45.1	43.6	40.0	38.1	34.4	33.7	32.5	30.8	30.5	29.7	29.5	29.1	29.0	28.7	28.5	28,3	28.0	27.8	27.8	27.7	27.6
	Score	928	694	694	598	573.5	547.5	546.5	535.5	506.5	489.5	449	427.5	386	378	365	345.5	342.5	333.5	331.5	326	325.5		320	317	314	312	312	311	310
	Result No.		7	m	4	'n	9	7	80	6	10	#	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

angiotensin II rec angiotensin II rec	H	angiotensin II rec	G protein-coupled	interferon-inducib	angiotensin II rec	G protein-coupled	somatostatin recep	somatostatin recep	interleukin-8 rece	brain-specific som	somatostatin recep	interleukin-8 rece	somatostatin recep	interleukin-8 rece
JH0621	S44425	JQ1516	JN0621	JE0349	JN0694	I65989	157955	JN0763	A48921	A47249	JN0605	A53611	I57940	J01231
9.0	1 (2)	~	~1	7	~1	7	N	~	~	~	N	7	~	7
359	359	359	350	367	362	333	363	364	359	384	388	360	363	355
27.5	27.4	27.3	25.9	25.6	25.2	24.6	24.6	24.6	24.5	24.4	24.1	24.0	23.8	23.6
309	307	306	291	287.5	283	276	276	276	274.5	273.5	270.5	269	267	265

ALIGNMENTS

RESULT 1 A43113

CremoXine (-c.) receptor 3 minimum	
N;AITEIDATE DAMES: C-C CAR-3; CCR3	
C;Species: Homo sapiens (man)	
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000	
C; Accession: A43113; S71808; A58834; A58832; G02653; A58833	
R;Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentler, M.	
Biochemistry 35, 3362-3367, 1996	_
A; Title: Molecular cloning and functional expression of a new human CC-chemokine rece	
A; Reference number: A43113; MUID: 96241590; PMID: 8639485	
A; Accession: A43113	
A; Molecule type: mRNA	
A; Residues: 1-352 <sam1></sam1>	
A; Cross-references: GB: X91492; NID: q1262810; PIDN: CAA62796.1; PID: 91262811	
R; Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Sarac	
M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.;	
Nature 382, 722-725, 1996	
A; Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant allele	
A; Reference number: S71808; MUID:96345670; PMID:8751444	
A: brossion: 571808	

G.) elé

A/Accession: 5/1000 A/Status: nucleic acid sequence not shown; not compared with conceptual translation A; Molecule type: DNA

A; Residues: 182-206; 207-230 <SAM2>
A; Recession: A58834
A; Recession: A58834
A; Residues: 182-206; 207-230 <SAM2>
A; Recession: A58834
A; Status: nucled ca cid sequence not shown; not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 1-184, 'IKDSHIGAGPARACHGHILLGNPKNSASVSK' <SAM3>
A; Cross-references: GB:X99333; NID:g1524062; PIDN:CA67767.1; PID:g1524063
A; Note: this frameshift mutation results in a non-functional receptor but confers a (nd may have had a selective advantage by conferring resistance to Yersinia plaque in: R; Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.
J. Leukoc. Biol. 60, 147-152, 1996
A; Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine A; Reference number: A58832; MUID:96295970; PMID:8699119

A; Residues: 1.152 < COM1>
A; Cross-references: GOM1>
A; Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes R; Combadiere, C. submitted to the EMBL Data Library, May 1996
A; Reference number: H01541
A; Accession: G02653

A;Accesson: usuals are from GB/EMBL/DDBJ
A;Kolecule type: mRNA
A;Wolecule type: mRNA
A;Wolecule type: mRNA
A;Redecule :1-352 <CCOM2>
A;Redecule :1-352 <CCOM2>
A;Cross-references: EMBL:U57840
B;Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 1716-17166, 1996
A;Hitle: Molecular cloning and functional characterization of a novel human CC chemol A;Reference number: A58833; MUID:96291862; PMID:8663314

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A Map position: 3p21-3p21

C; Superfamily: vertebrate rhodopsin

C; Superfamily: vertebrate rhodopsin

C; Superfamily: vertebrate rhodopsin

C; Superfamily: vertebrate rhodopsin

C; Star alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane #status predicted <TM2>
F; 19-99/Domain: transmembrane #status predicted <TM3>
F; 154-178/Domain: transmembrane #status predicted <TM3>
F; 154-178/Domain: transmembrane #status predicted <TM5>
F; 208-225/Domain: transmembrane #status predicted <TM6>
F; 222-309/Domain: transmembrane #status predicted <TM6>
F; 222-309/Domain: transmembrane #status predicted <TM6>
F; 222-309/Domain: transmembrane #status predicted <TM6>
F; 242-309/Domain: transmembrane #status predicted <TM6-309/Domain: transmembrane #status
                                 Aymap position: 3p21-3p21
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate respective developed cross-specification of the state o
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E; Accession: 138450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 INLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129
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C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 YDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILLLINCKRLKSMTDIYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 61.9%; Score 694; DB 2; Best Local Similarity 75.9%; Pred. No. 2.4e-56; Matches 132; Conservative 17; Mismatches 23.
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A;Cross-references: GDB:337364; OMIM:601267
A; Cross-references: GDB:337364; OMIM:601267
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A;Molecule type: mRNA
A;Residues: 1-374 <RES>
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Matches 132;
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R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A;Title: Nulecular cloning and functional expression of two monocyte chemoattractant pro
A;Reference number: A53477; MUID:94195821; PMID:8146186
A;Accession: I38463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Description: G protein-coupled receptor for chemokines MIP-lalpha, MIP-lbeta and RANTH A Note: probably acts to control granulocyte proliferation and differentiation c; Superfamily: vertebrate rhodopsin c; Superfamily: vertebrate rhodopsin c; Superfamily: vertebrate rhodopsin c; Superfamily: vertebrate rhodopsin respector; glycoprotein; phosphoprotein; transmembrane status predicted <TM2> F: 32-56/Domain: transmembrane status predicted <TM3> F: 124-166/Domain: transmembrane status predicted <TM4> F: 141-166/Domain: transmembrane status predicted <TM5> F: 183-218/Domain: transmembrane status predicted <TM5> F: 185-30/Domain: transmembrane status predicted <TM6> F: 185-30/Domain: transmembrane status predicted <TM6> F: 236-251/Domain: transmembrane
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Milternate names: C-C CRT-2; monocyte chemoattractant protein 1 receptor; monocyte chem
C:Species: Homo sapiens (man)
C;Detcies: Homo sapiens (man)
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rjamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
Blochem. Blophys. Res. Commun. 202, 1156-1165, 1994
A;Title: CDNA. Clonida and functional expression of a human monocyte chemoattractant prot
A;Reference number: JC2443; MUID:94324942; PMID:8048929
                                                  A;Cross-references: GB:U54994; NID:g1457945; PIDN:AAC5059B.1; PID:g1457946
C;Comment: This is a receptor for chemokines MIP-lalpha (see PIR:A30574), MIP-lbeta (see C;Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                            C;Genetics:
A;Gene: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CKR5; ChemR13
A;Cross-references: GDB:1230510; OMIM:601373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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C; Function:
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A; Residues: 1-360 < YAM>
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A; Residues: 1-360 <RES>
     A; Molecule type: mRNA
A; Residues: 1-352 <RAP>
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HFPY 184
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Matches 184
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C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane pr.40-65/Domain: transmembrane #status predicted <TM1>
F;76-97/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chemokine (C-C) receptor 4 - human
N'Alternate names: C-C CKR-4
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #text_change 21-Jul-2000
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.
J. Biol. Chem. 270, 19495-19500, 1995
A;Title: Molecular cloning and functional expression of a novel CC chemokine recepton A; Reference number: A57160; MuID:95370289; PMID:7642634
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                                                                                                                                                                                                 A;Reference number: 149339; MUID:95340546; PMID:7542241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 DINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLL 70
                                         macrophage inflammatory protein-1 alpha receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: 14939
C;Accession: 14939
B;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Wolecule type: DNA
A;Rosadues: 1-355 cR82
A;Rosadues: L-355 cR82
A;Cross-references: EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548
C;Superfamily: vertebrate rhodopsin
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A;Residues: 1-360 <POW>
A;Cross-references: GB:X85740; NID:q1370103; PIDN:CAA59743.1; PID:g971452
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A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 61.19
Matches 107; Conservative
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R;Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
A;Title: Nolecular cloning, functional expression, and signaling characteristics of a C-A;Reference number: A45177; MUID:93161416; PMID:7679328

    Exp. Med. 177, 1421-1427, 1993
    Aritle: Structure and functional expression of the human macrophage inflammatory 1 alph
A;Reference number: 155671; MUID:93240122; PMID:7683036

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F:108-129/Domain: transmenbrane fstatus predicted <TM4>
F:140-121/Domain: transmenbrane fstatus predicted <TM4>
F:240-25-223/Domain: transmembrane fstatus predicted <TM5>
F:240-264/Domain: transmembrane fstatus predicted <TM5>
F:288-305/Domain: transmembrane fstatus predicted <TM7>
F:588-305/Domain: transmembrane fstatus predicted <TM7>
F:581-305/Domain: transmembrane fstatus predicted <TM7>
F:542-273,106-183/Disulfide bonds: #status predicted
F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Reywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; F;36-60/Domain: transmembrane #status predicted <TM1>
F;71-91/Domain: transmembrane #status predicted <TM2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chemokine (C-C) receptor 1 - human
NyAlternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
C:Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 DYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A. Molecule type: mRNA
A. Residues: 1-355 <NEO>
A. Cross-references: GB:L10918; NID:9292416; PIDN:AAA36543.1; PID:9292417
                                                                                        130 VVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSOKEGLHYTCSSHFP 183
                                                                                                                           A; Cross-references: GB:L10918; NID: 9292416; PIDN: AAA36543.1; PID: 9292417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Experimental source: HL60 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:124876)
R;Gao, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.3%; Score 598; DB 2;
59.2%; Pred. No. 1.6e-47;
tive 34; Mismatches 37;
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A,Status: preliminary: translated from GB/EMBL/DDBJ
A,Molecule type: mRNB
A,Residues: 1-355 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDB:138446; OMIM:601159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: nucleic acid sequence not shown
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A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
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Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: GDB: CMKBR1; CMKR-1
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186 нгрн 189
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A Map position: 3p21-3p21
C; Superfamily: vertebrate rhodopsin
C; Stoperfamily: vertebrate rhodopsin
F; 371-91, Domain: transmenbrane #status predicted <TM2>
F; 371-91, Domain: transmenbrane #status predicted <TM3>
F; 301-23, Domain: transmembrane #status predicted <TM5>
F; 205-223, Domain: transmembrane #status predicted <TM5>
F; 205-223, Domain: transmembrane #status predicted <TM5>
F; 205-223, Domain: transmembrane #status predicted <TM5>
F; 346-251, Domain: transmembrane #status predicted <TM5>
F; 346-37, Job. 183, Disaulfide bonds: #status predicted <TM7>
F; 345-78 inding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Combadiere, C.; Ahuja, S.K.; Murphy, P.M.
J. Biol. Chem. 270, 16491-16494, 1995
J. Biol. Chem. 270, 16491-16494, 1995
J. Hiol. Chem. 270, 16491-16494, 1995
J. Hiol. Chem. 270, 16491-16494, 1995
J. Mill. Chem. 270, 16491-16494
J. Reference number: A57237; MUID:95348056; PMID:7622448
A; Accession: A57237
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A;Note: the translated sequence in Genbank entry HSU28694, release 113.0, PIDN:AAC504
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                                                                                                                                                                                                                                                                                                                              74 ISDLFFLLTVPFWAHYAA-AQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLAVVH 132
                                                                                                                                                                                                                                                                                                                                                                                     82 ISDLLFLFTVPFWIHYVLWNEWGFGHYMCKMLSGFYYLALYSEIFFIILLTIDRYLAIVH 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 COKINVKOIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLLNLAISDLFF 79
                                                                                                                                                                                                                                                                        81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A. Molecule type: DNA
A. Residues: 1-355 <PONN>
A. Cross-references: EMBL: U49727; NID: 91477560; PIDN: AAB09726.1; PID: 91477561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Species: Homo sapiens (man)
C.Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000
C.Accession: 402436; A57237
C.Rochath, P.D.
Submitted to the EMBL Data Library, February 1996
                                                                                                                                                                                                                 14 YYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLLNLA
                                                                                                                                                                                                                                               22 YEWAPPCEKVRIKELGSWILPPLYSLYFIIGLIGNMWYVILILIKYRKLQIMINIYLENLA
                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 AVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFP 183
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                                                                                                 Length 359;
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                                                                                                                                                          Indels
A;Gross-references: EMBL:U28406; NID:9881551; PID:9881552 C;Superfamily: vertebrate rhodopsin
                                                                                        ch 47.7%; Score 535.5; DB 2;
l Similarity 57.9%; Pred. No. 9e-42;
99; Conservative 31; Mismatches 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: GDB:CMKBR3
A;Cross-references: GDB:579624; OMIM:601268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: nucleic acid sequence not shown
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A; Accession: G02436
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                                                                                           Query Match
Best Local Si
Matches 999
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Keywords: glycoprotein; phosphoprotein; receptor; thymus
3,134,214,214diding alte: carbonydrate (Asn) (covalent) *status predicted
7,22,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) *status predistably Caralent) (By protein kinase C) *status predicted
3,321/Binding site: phosphate (Ser) (covalent) (by protein kinase C) *status predicted
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 0.2 Uul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998
C;Accession: 149341
R;Gao, J.L.; Murphy, P.M.
B;Gao, J.L.; Murphy, P.M.
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemoki A;Reference number: 149339; MUID:95340546; PMID:7542241
A;Accession: 149341
A;Accession: 149341
A;Molecule type: DNA
A;Residues: 1-359 <RES>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C;Accession: 174587
R;Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines 1A;Accession: JC4587; MUID:96136324; PMID:8573157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 DIYILULAISDLFFILITVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTID 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 DVYLLNLAISDLLFVLSLPFWGYYAADQWVFGLGLCKIVSWMYLVGFYSGIFFIMLMSID 134
                                                                                                                                                       CKRLKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIF 117
                                                                                                                                                                                         FIILLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYT 177
                                                                                                                                                                                                                                                                                                         9 IYDINYY---TSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DYQVSSPIYDINYYTSE----PCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILIN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: EMBL: X90862; NID: 91167851; PIDN: CAA62372.1; PID: 91167852
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55.9%; Pred. No. 8.8e-43;
1ve 36; Mismatches 39;
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Best Local Similarity
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A; Residues: 1-360 <HOO>
                                                                                                                                                                                                                                                                                                                                                                                        CSSHF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                            CKTKY 191
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C; Superfamily: ve
C; Keywords: glyco
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G protein-coupled receptor CKR-L1 - human
N;Alternate names: chemokine receptor-like protein TER1; GPR-CY6
C;Species: Homo saplens (man)
C;Date: 31-Jan-1997 #sequence.revision 31-Jan-1997 #text_change 21-Jul-2000
B;Caballos, A; Varona, R; Gutierrez, J; Lind, P; Marquez, G.
B;Caballos, A; Varona, R; Gutierrez, J; Lind, P; Marquez, G.
B;Caballos, A; Varona, R; Gutierrez, J; Lind, P; Marquez, G.
B;Caballos, A; Varona, R; Gutierrez, J; Lind, P; Marquez, G.
B;Caballos, A; Varona, R; Gutierrez, J; Lind, P; Marquez, G.
B;Caballos, A; Varona, R; Gutierrez, J; Lind, P; Marquez, G.
B;Caballos, A; Varona, R; Gutierrez, J; Lind, P; Marquez, G.
B;Caballos, A; Varona, R; Gutierrez, J; Lind, P; Marquez, G.
B;Caballos, A; Varona, R; Gutierrez, J; Lind, P; Marquez, G.
B;Caballos, A; Varona, R; Gutierrez, J; Lind, P; Marquez, G.
B;Caballos, A; Varona, R; Gutierrez, J; Lind, P; Marquez, G.
B;Caballos, A; Varona, R; Gutierrez, J; Lind, P; Marquez, G.
B;Caballos, A; Varona, R; Gutierrez, J; Lind, P; Marquez, G.
B;Caballos, A; Varona, R; Gutierrez, J; Lind, P; Marquez, G.
B;Caballos, A; Varona, R; Gutierrez, J; Lind, P; Marquez, G.
B;Caballos, A; Varona, R; Gutierrez, J; Lind, P; Marquez, G.
B;Caballos, A; Varona, R; Gutierrez, J; Lind, P; Marquez, G.
B;Caballos, A; Varona, R; Gutierrez, J; Lind, P; Marquez, G.
B;Caballos, A; Varona, R; Gutierrez, J; Lind, P; Marquez, G.
B;Caballos, A; Varona, R; Gutierrez, G.
B;Caballos, Gutierrez, Gutierr
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A; Residues: 1-355 c.ZAB>
A; Residues: 1-355 c.ZAB>
A; Residues: Leftences: EMBL: Z/9782; NID:g1668735; PIDN:CAB02142.1; PID:g1668736
R; Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A. submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 IFFIILLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLH 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDYTLDLSVTTVTDYXYPDIFSSPCDAELIQTNGKLLAAVFYCLLFVFSLLGNSLVILVL 60
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C;Comment: This protein belongs to the family of beta chemokine receptors.
                                                                                  227
129 AVVHAVFALKARTVTFGVYTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFP 183
                                                  5,
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A;Molecule type: DNA
A;Residues: 1-355 <NAP>
A;Cross-references: EMBL:U62556; NID:q1468978; PID:q1468979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribonner, T.I.
submitted to the EMBL Data Library, January 1996
submitted to the EMBL Data Library, January 1996
A; Reference number: H01154
A; Accession: G02387
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Rolecule type: DNA
A; Redidues: 1-355 < BON>
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A;Cross-references: GDB:6053733; OMIM:601834
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C; Superfamily: vertebrate rhodopsin
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A; Accession: G02776
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C;Date: 02-014-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: 149340
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17444-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemoki A;Title: Cloning and differential tissue-specific expression of three mouse beta chemoki A;Reference number: 149339; MUID:95340546; PMID:7542241
A;Accession: 149340
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 ILLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCS 179
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C;Species: equine herpesvirus 2
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
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C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor
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R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A;Titler The DNA sequence of equine herpesyirus 2.
A;Reference number: 555594; MUID:95302501; PMID:7783207
A;Accession: S55594
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                                                  ARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 43.6%; Score 489.5; DB 2;
1 Similarity 51.1%; Pred. No. 1.5e-37;
94; Conservative 34; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.0%; Score 449; DB 2;
48.6%; Pred. No. 8.7e-34;
tive 37; Mismatches 51.
                                                                                                                                                                                                                                                                                                                                                            C; Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                   MIP-1 alpha receptor like-1 - mouse
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A; Residues: 1-383 <TEL>
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Best Local Si
Matches 94;
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         139
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S55594
                                                                                                                                                                                                                            RESULT 10
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Matches 73
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probable G protein-coupled receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: 158186
R;Harrison, J.K.; Barber, C.M.; Lynch, K.R.
Marrison, J.K.; Barber, C.M.; Lynch, K.R.
Marrison, J.K.; Barber, C.M.; Lynch, R.R.
Marrison, J.K.; Barber, C.M.; Lynch, R.R.
My Title: CDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and ka;Reference number: 158186
My Reference number: 158186
My Reference number: 158186
My Reference number: 158186
My Residues: 1-354 CRES
A;Residues: 1-354 CRES
A;Cross-references: EMBL:U04808; NID:92558635; PIDN:AAB87093.1; PID:g439861
C;Superfamily: vertebrate rhodopsin
C;Reywords: G protein-coupled receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 KSMTDIYLLINLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIIL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSH 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                6 SSPIYDINYY----TSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: JC5942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPPELDLENFEYDDSAEACYLGDIVAFGTIFLSIFYSLVFTFGLVGNLLVVIALTNSRKS
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E;Accession: JC5942
Biochem. Biophys. Res. Commun. 243, 264-268, 1998
A;Title: Cloning and characterization of a novel human chemokine receptor. A;Reference number: JC5942; MUID:98139902; PMID:9473515
A;Accession: JC5942
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:U97123; NID:92897070; PIDN:AAC39595.1; PID:92897071
C;Superfamily: vertebrate rhodopsin
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                                                                                                                                                                                                                                                                                                                                               Length 354;
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...hos 67; Indels
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                                                                                                                                                                                                                                                                                                                                             34.4%; Score 386; DB 2; 42.4%; Pred. No. 5e-28;
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                                                                                                                                                                                                                                                                                                                                                                                     78; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   42.48;
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Best Local Similarity
Matches 78; Conserv
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YPEV 183
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Matches
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C;Species: Homo sapiens (man)
C;Species: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
C;Accession: UC4304
R;Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 295-299, 1995
Gene 163, 295-299, 1995
A;Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related the A;Reference number: UC4304; MUID:96011651; PMID:7590284
                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-355 < RAP>
A; Residues: 1-355 < RAP>
A; Cross-references: GB-120350; NID:9665580; PIDN:AAA91783.1; PID:9665581
A; Cross-references: GB-120350; NID:9665580; PIDN:AAA91783.1; PID:9665581
C; Comment: This portein is a cell-surface receptor which recognizes extracellular sig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 LEFLLITVPFWAHYAAAQWDFGNTMCQLLIGLYFIGFFSGIFFIILLIIDRYLAVVHAVFA 136
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C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate properties transmembrane fistatus predicted <TML>
F;35-57/Domain: transmembrane fistatus predicted <TM2>
F;66-88/Domain: transmembrane fistatus predicted <TM3>
F;104-125/Domain: transmembrane fistatus predicted <TMA>
F;197-217/Domain: transmembrane fistatus predicted <TMA>
F;230-254/Domain: transmembrane fistatus predicted <TMA>
F;230-254/Domain: transmembrane fistatus predicted <TMA>
F;230-254/Domain: transmembrane fistatus predicted <TMA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.5%; Score 365; DB 2; Length 355; 43.2%; Pred. No. 4.3e-26; Live 28; Mismatches 64; Indels
orphan G protein-coupled receptor - human
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                                               N; Alternate names: V28 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                            A; Accession: JC4304
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Search completed: June 3, 2003, 19:24:27 Job time: 24.5976 secs Human protease #2.
Human G protein-co
Propionibacterium
Human protease #1.
Human protease #3.

Human ovarian anti

Drosophila melanog Human metalloprote

Human protease PRT

Human protein NOV1 Human protease #7.

protease #6 Human protease #5

Human 1

Novel human diagno Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia

Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Drosophila melanog Human polypeptide

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Human protease #4. Human metalloprote Human ADAM-TS 1 pr Human protease #9. Human protease #8.

protease #10 human diagno

Human | Novel |

Human protease #11

Orosophila melanog

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Inactive, human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2; predisposition; resistance; diagnosis; treatment; prevention; inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthmis; idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer; atherosclerosis; autoimmune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vassart G;
                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                    AAU77124
AAU77124
ABB63141
AAU72895
AAU74750
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AAU77128
AAU77127
AAU77126
AAU77126
AAU77125
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AAU77129
AAU77129
AAU77132
AAU77131
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AAU40849
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96EP-0870021.
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(first entry)
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(EURO-) EUROSCREEN SA
                                                                                                                                                                                                                                                                                                                                                                                                                                        Inactive human CCR5.
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Homo sapiens
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                                           AAW27408;
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HIV-1 co-receptor
Peptide #4504 enco
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human diagno
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                                                                       (without alignments)
520.312 Million cell updates/sec
                                                                                                                                                                                                                                                                      1: /SIDSZ/gcgdata/geneseg/genesegp-embl/AA1980.DAT:*
2: /SIDSZ/gcgdata/geneseg/genesegp-embl/AA1981.DAT:*
3: /SIDSZ/gcgdata/geneseg/genesegp-embl/AA1983.DAT:*
3: /SIDSZ/gcgdata/geneseg/genesegp-embl/AA1983.DAT:*
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7: /SIDSZ/gcgdata/geneseg/genesegp-embl/AA1985.DAT:*
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7: /SIDSZ/gcgdata/geneseg-embl/AA1988.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:
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                                                              3, 2003, 19:17:26 ; Search time 7.93902 Seconds
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         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                           164
1 ikdshlgagpaaachghlllgnpknsasvsk 31
                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                  US-09-938-703-6_COPY_185_215
                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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AAM57726
AAM70138
ABG39777
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ABB69618
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ABG27246

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Match 1
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This is the amino acid sequence of a CCR5 variant protein, designated CCR5-delta32, that includes the first 4 transmembrane commains of wild-type CCR5 (see AAW8821), but lacks transmembrane domains 5-7. CCR5 serves as a co-receptor for infection by macrophage-tropic (M-tropic) strains of HIV-1. Individuals chancinguals for the CCR5-delta32 mutation are resistant to HIV-1 infection, but heterozygous individuals are susceptible. The circomic additionally relates to the identification of variant correction, but heterozygous individuals are susceptible. The cross of the correction of variant corrections and the correction of cCR5-delta32 mutations may be used to identify individuals at lower risk of infection relative to the general copulation who, if infected, may exhibit slower progression to AIDS. Probes and primers (see AAW8127-36) are provided for use in diagnostic methods for detecting the presence of such variants. A method is provided for inhibiting HIV-1 infection of a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                        expressing the CCR5 receptor. This involves introducing a nucleic acid encoding a CCR5 variant into the cell, thereby reducing the number of functional CCR5 molecules present on the cell surface.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide #4504 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 29633; 639pp + sequence listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 164; DB 20;
Pred. No. 4.7e-15;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     analyzing gene expression in human fetal liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 164; D
Best Local Similarity 100.0%; Pred. No. 4.7
Matches 31; Conservative 0; Mismatches
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Disclosure; Page 38-39; 55pp; English.
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2000US-0608408.
2000US-0632366.
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2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                       215 AA;
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                        The present sequence is an inactive human CC (Cys-Cys) chemokine receptor 5 (CCR5), which lacks the last 3 transmembrane regions and the regions involved in G protein-coupling. CCR5 or its cDNA can used to disgnose, treat and/or prevent inflammatory diseases, e.g. rheumatodia trinfils, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis, viral infections, especially human immunodeficiency virus type 1 or type 2 (HIV-1 or HIV-2) infection, cancer, atheroscierosis and autoimmune disorders. Subjects that express the inactive receptor have a predisposition, or resistance to HIV-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIV+1; CCR5; CCR5-delta32; co-receptor; infection; diagnosis; AIDS;
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                                       Active and inactive forms of human CC chemokine receptor CCR-5 useful to diagnose, prevent and/or treat inflammatory disorders, autoimmune disease and viral infection
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                                                                                                                                                                                                                                                                                                                                                                                                                          Length 215;
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                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 164; DB 18; 100.0%; Pred. No. 4.7e-15;
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hte= "transmembrane domain 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV-1 co-receptor CCR5 variant CCR5-delta32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IKDSHLGAGPAAACHGHLLLGNPKNSASVSK 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                       Claim 7; Fig 1d-e; 94pp; English
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142..167
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67..87
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103..12
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Best Local Similarity
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    N-PSDB; AAT90118.
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Domain
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may can ble the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human peptide encoded by genome-derived single exon probe SEQ ID 29442.
                                                                                                                                                                                                                                                                  Human bone marrow expressed probe encoded protein SEQ ID NO: 30444.
                                                                                                                                                                                                                                                                                                   Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analyzing gene expression in human bone marrow
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Pred. No. 3.3;
1; Mismatches
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|DSHLGGGPAATA-----GGPRTS 65
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50.0%;
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Matches 12; Conservative
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27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human brain expressed single exon probe encoded protein SEQ ID NO: 29831.
liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single exon nucleic acid probes for analyzing gene expression in human
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                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO: 29831; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22; Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                         DB 22; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 3.3;
1; Mismatches
                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 55;
Pred. No.
                                                                                                                                                                                         Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rank DR;
                                                                                                                                                                                                                                                                                         3 DSHLGAGPAAACHGHLLLGNPKNS 26
                                                                                                                                                                                                                                                                                                                                                                                               AAM57726 standard; Protein; 84 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0234687.
2000US-0236359.
2000GB-0024263.
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50.0%;
                                                                                                                                                                                         33.5%;
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2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20000S-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20000S-0632366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                         Query Match 33.55
Best Local Similarity 50.05
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 AA;
                                                                                                                                                      84 AA;
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21-SEP-2000; 27-SEP-2000; 04-OCT-2000;

brains

Sequence

Query Match Best Local S Matches 12

04-FEB-2000;

26-MAY-2000; 30-JUN-2000; 33-AUG-2000;

Homo sapiens

09-AUG-2001

05-NOV-2001

AAM57726;

RESULT 4
AAM57726

셤 ð

1;

Gaps

6

5;

Length 84; Indels

DB 22;

Spatially-addressable set of single exon nucleic acid probes, used to Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idioperhic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; gaucher's disease; Nlemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary hashocytosis; lymphanglolenowynomicsis; Raragener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dyskinesis; pulmonary dyskinesis; pulmonary dyskinesis; pulmonary hypertension; Rank DR; (MOLE-) MOLECULAR DYNAMICS INC. Penn SG, Hanzel DK, Chen W, 2000US-236359P. 2000GB-0024263. 2000US-0608408 2000US-0632366. 2000US-234687P. 30-JAN-2001; 2001WO-US00665 2000US-180312P hyaline membrane disease. WPI; 2002-114183/15 WO2001B6003-A2. 21-SEP-2000; 27-SEP-2000; 04-OCT-2000; Homo sapiens. 04-FEB-2000; 26-MAY-2000; 30-JUN-2000; 03-AUG-2000; 15-NOV-2001.

measure gene expression in human lung samples Claim 27; SEQ ID No 29442; 634pp; English.

The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived concleic acid probes form measuring sene expression in a sample derived from human lung comprising the probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung comprising (a) algorithmically predicting at least one exon from genomic sequences of the array; identifying exons in a enkaryotic genome, comprising cat algorithmically predicting at least one exon from genomic sequences of the array and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung maRNA, to a single exon probe, having a fragment identifying exons from genomic sequence some mentioned microarray; assigning exons to a single exon in the above mentioned microarray; assigning exons to a single exon in the above mentioned microarray; assigning exons to a single exon comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon expression of the exons in the tissues and/or cell types using hybridisation, or encoded by the expression of the exons should be assigned to a single gene; a peptide comprising one comprising human lung derived mana and for the study of lung diseases

C 12011 sequences, mentioned in the specification, or encoded by the expression analysis, and for identifying exons in a gene, particularly using human lung derived mana expression and passe (llb), familiarly idiopathic pulmonary high charansky-pulmonary is unlanged. The probes to haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating considers involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and call and oacid sequences. ABSG00010-BBS30377 represent novel human
                                                                                                                                                                                            Ξ,
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                            9:
encoded by a single exon probe of the invention.

Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic
format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                    33.5%; Score 55; DB 23; Length 84; 50.0%; Pred. No. 3.3; 1, Wismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID No 54232; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human diagnostic protein #23864.
                                                                                                                                                                                                                                                                     65
                                                                                                                                                                                                                                   3 DSHLGAGPAAACHGHLLLGNPKNS 26
                                                                                                                                                                                                                                                           48 DSHLGGGPAATA----GGPRTS
                                                                                                                                                                                                                                                                                                                                                                    ABG23873 standard; Protein; 94 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-0540217, 23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                               18-FEB-2002 (first entry)
                                                                                                                                                                          Best_Local Similarity 50.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-639362/73.
N-PSDB; AASB8060.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                 84 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-0CT-2001.
                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                           ABG23873;
                                                                                                                                                        Query Match
                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                RESULT 7
                                                                                                                                                                                                                                                                                                                                                  ABG23873
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The colynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations are possible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 53.5; DB 22;
Pred. No. 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KDSHLGAGPAAACHGHLLLGNP--KNSASVSK 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID No 58129; 103pp; English.
                                                                                                                                                                                                                   Novel human diagnostic protein #27761.
                                                                                  ABG27770 standard; Protein; 189 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0540217.
2000US-0649167.
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                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-639362/73.
N-PSDB; AAS91957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                      W0200175067-A2.
                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000;
23-AUG-2000;
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                                                                                                                                                                         18-FEB-2002
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                                                                                                                              ABG27770;
                                           RESULT 9
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                                                                                                                                                                         1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                         9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 35646; 21pp + Sequence Listing; English
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                                                                                                                         Score 55; DB 22; Length 94;
Pred. No. 3.8;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 35646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 GAGPAAACLAVCCSPGSSHHHLGHVGHLATGHP 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----H-GHLLLGNP 23
                                           at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                       3 DSHLGAGPAAACHGHLLLGNPKNS 26
                                                                                                                                                                                                                                                              DSHLGGGPAATA----GGPRTS 50
                                                                                                                                                                                                                                                                                                                                                                        ABB69618 standard; Protein; 276 AA.
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2000US-0614150.
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                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-656860/75.
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es 14; Conserv
                                                                                                                                                     Best Local Similarity
Matches 12; Conserv
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                                                                                       94 AA;
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23-MAR-2000; 11-JUL-2000;

Venter JC,

27-SEP-2001.

interactions

pharmaceutical

26-MAR-2002

ABB69618;

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셤 ð

RESULT 8

Sequence

Query Match

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ä

10;

Length 189; Indels

Seguence

Query Match

Best Loc Matches

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ABG27246;

RESULT 10 ABG27246

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 19466.
AAG18166 standard; Protein; 216 AA.
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9905-0132486.
9905-0132486.
9905-0132421.
9905-0134218.
9905-0134218.
9905-013421.
9905-0134370.
9905-0134370.
9905-0135353.
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99US-0130891.
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99US-0132407.
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99US-0139454.
99US-0139455.
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99US-0123180.
99US-0123548.
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                                                                          17-0CT-2000 (first entry)
                                                                                                                                                                                                                                Arabidopsis thaliana
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18-JUN-1999;
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30-APR-1999;
04-MAY-1999;
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14-MAY-1999;
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28-APR-1999;
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                                      AAG18166;
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymeptide (II) sequences. (I) is useful as hybridisation probes, and for chromosome and gene mapping, and in recombinant production of (II). The colynucleotides are also used in diagnostics as expressed sequence tags of identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or exportance and as a food supplement. (II) and its binding partners are useful for treating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating anging of sites expressing (II). (I) and (II) are useful for treating anging of sites expressing (II). (I) and (II) are useful for treating asorther involved and asorther are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating a food supplement. (III) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating a food supplement. (III) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating a food supplement. (III) and its binding partners are useful in medical diagnostics, forensics, gene mapping, identification of mutations are sponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABGOOULD-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                     Novel human diagnostic protein #27237,
                                    ABG27246 standard; Protein; 197 AA.
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23-AUG-2000; 2000US-0649167.
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Sequence

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RESULT 11

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Arabidopsis thaliana protein fragment SEQ ID NO: 19465.
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99US-0157753.
99US-0157865.
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Gaps 7

Length 216; Indels

21; BB

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence. Arabidopsis thaliana. BED1033405-A2. 06-SEP-2000. 25-FEB-2000; 2000EP-0301439.	
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                                                                                                                                                                                                                                                                                                                                                                                                                            th 32.0%; Score 52.5; I Smilarity 45.5%; Pred. No. 28; 10; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 RNDNNGYGPPGG-HGHLMAGNP 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG28063 standard; Protein; 270 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KDSHLGAGPAAACHGHLLLGNP 23
                                                                                                                                                                                                                                                                                                                                                                 99US-0161360.
99US-0161361.
99US-0161920.
99US-0151438.
99US-0152363.
99US-0152363.
99US-0153070.
99US-0154018.
99US-0154018.
99US-0154019.
99US-0154019.
99US-0155139.
99US-0155139.
99US-0155486.
99US-0155486.
99US-0155486.
99US-0155486.
99US-0155486.
99US-0155486.
99US-015929.
99US-015929.
99US-015929.
99US-015929.
99US-015929.
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99US-0160767.
99US-0160768.
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99US-0160980.
99US-0160981.
99US-0160989.
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99US-0161406.
99US-0161359.
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99US-0161993.
99US-0162142.
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99US-0160814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
31-AUG-1999;

01-SEP-1999;

10-SEP-1999;

11-SEP-1999;

15-SEP-1999;

20-SEP-1999;

21-SEP-1999;

22-SEP-1999;

24-SEP-1999;

24-SEP-1999;

24-SEP-1999;

04-CCT-1999;

06-CCT-1999;

07-CCT-1999;

13-CCT-1999;

13-CCT-1999;

14-CCT-1999;

15-CCT-1999;

16-CCT-1999;

17-CCT-1999;

17-CCT-1999;

18-CCT-1999;

18-CCT-1999;

18-CCT-1999;

18-CCT-1999;

18-CCT-1999;

18-CCT-1999;

18-CCT-1999;

21-CCT-1999;
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28-OCT-1999;
29-OCT-1999;
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                                                                                                                                                                                                                                                                           21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
                                                                                                                                                                                                                                                                                                                                               25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
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Best Local Si
Matches 10;
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990S-0154779.
990S-01558139.
990S-0155686.
990S-0155658.
990S-0156458.
990S-0157117.
990S-01577173.
990S-0158029.
990S-0158029.
990S-0158029.
990S-0158369.
990S-0159339.

990S-0159637. 990S-0159638. 990S-0159584.

99US-0160815. 99US-0160980. 99US-0160981.

99US-0160989. 99US-0161404. 99US-0161405.

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990S - 0142154.
990S - 0142154.
990S - 0142390.
990S - 0142803.
990S - 0142977.
990S - 0143542.
990S - 0144332.
990S - 0144332.
990S - 0144333.
990S - 0144614.
990S - 014508.
990S - 014508.
990S - 0145192.
990S - 0145192.
990S - 0145513.
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990S-0147935.
990S-0148171.
990S-0148319.
990S-0148341.
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990S-0149368.
990S-0149175.
990S-0149722.
990S-0149722.
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990S-0149902.
990S-0149930.
990S-0150566.
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01-JUL-1999;

02-JUL-1999;

06-JUL-1999;

09-JUL-1999;

11-JUL-1999;

12-JUL-1999;

12-JUL-1999;

13-JUL-1999;

13-JUL-1999;
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12-AUG-1999;
13-AUG-1999;
13-AUG-1999;
17-AUG-1999;
17-AUG-1999;
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20-AUG-1999;
20-AUG-1999;
23-AUG-1999;
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31-AUG-1999;
01-SEP-1999;
07-SEP-1999;
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25-AUG-1999;
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02-AUG-1999;
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06-AUG-1999;
06-AUG-1999;
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09-AUG-1999;
10-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-AUG-1999
                                                                                                                                                                                                                                                                                                                02-AUG-1999
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 32.0%; Score 52.5; DB 21; Local Similarity 45.5%; Pred. No. 28; hes 10; Conservative 4; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KDSHLGAGPAAACHGHLLLGNP 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
20-SEP-1999;
22-SEP-1999;
24-SEP-1999;
28-SEP-1999;
28-SEP-1999;
28-SEP-1999;
04-OCT-1999;
06-OCT-1999;
06-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
14-OCT-1999;
14-OCT-1999;
15-OCT-1999;
16-OCT-1999;
17-OCT-1999;
18-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG28062;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
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99US-0143624. 99US-0144005. 99US-0144085. 99US-0144086. 99US-0144331. 99US-0144333. 99US-0144334. 99US-0144334.	9905-0144884 9905-0144884 9905-0144884 9905-0145086 9905-0145087 9905-0145087 9905-0145192 9905-0145192 9905-0145192 9905-0145218 9905-0145218 9905-0145918 9905-0145918 9905-0145918	990S-014/038 990S-014/204 990S-014/305 990S-014/360 990S-014/360 990S-014/416 990S-014/416 990S-014/319 990S-0148341 990S-0148341 990S-0148341 990S-0148341 990S-0148341 990S-0148341 990S-0148341 990S-0148426	990x-0149229 990x-0149920 990x-0149930 990x-0150666 990x-0151065 990x-0151065 990x-0151080 990x-0151303 990x-0151303 990x-0151303 990x-0153780 990x-0153780 990x-0154779 990x-0154780 990x-0154780 990x-0154780 990x-0154780
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990S-0123180. 990S-0123548. 990S-0125788. 990S-012564. 990S-0126785. 990S-0128734. 990S-0128714. 990S-0128714.	990S-0130510. 990S-0131449. 990S-0131449. 990S-0132407. 990S-0132487. 990S-0132487. 990S-0132487. 990S-013486. 990S-013486. 990S-013487. 990S-0134718. 990S-0134718. 990S-0134718. 990S-0134718.	9905-013692. 9905-013692. 9905-013722. 9905-013722. 9905-013728. 9905-013724. 9905-0138540. 9905-0138540. 9905-013847. 9905-0139452. 9905-0139453. 9905-0139453. 9905-0139454.	99US-0139458. 99US-0139460. 99US-0139461. 99US-0139462. 99US-0139463. 99US-0139756. 99US-0139817. 99US-0140353. 99US-0140353. 99US-0140823. 99US-0140821. 99US-0141842. 99US-0141842. 99US-0141842. 99US-01418803. 99US-014287.
			8-JUN-1999; 8-JUN-1999; 8-JUN-1999; 8-JUN-1999; 8-JUN-1999; 8-JUN-1999; 8-JUN-1999; 8-JUN-1999; 8-JUN-1999; 1-JUL-1999; 8-JUN-1999; 1-JUL-1999; 8-JUL-1999; 8-JUL-1999; 8-JUL-1999; 8-JUL-1999; 8-JUL-1999; 8-JUL-1999; 8-JUL-1999; 8-JUL-1999; 8-JUL-1999; 8-JUL-1999; 8-JUL-1999; 8-JUL-1999; 8-JUL-1999; 8-JUL-1999; 8-JUL-1999; 8-JUL-1999; 8-JUL-1999; 8-JUL-1999; 8-JUL-1999;

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, collymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The collymerase chain in reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The collymeloctides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (II) is useful for gene therapy techniques concentrating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating care of supplement. (II) and its binding partners are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in the polypeptide and polynuclectide sequences have applications in the produce other types of darks and products dependent on DNA and cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of darks and products dependent on DNA and cannon acid sequences. Absolute Abertic and to produce other types of darks and products dependent on DNA and cannon acid sequences of the invention.

Consequence of the colling patent did not appear in the printed consequence of the invention of the colling of the col
                              New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
31.1%; Score 51; DB 22; Length 193;
Best Local Similarity 45.8%; Pred. No. 31;
Matches 11; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                         Claim 20; SEQ ID No 51392; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: June 3, 2003, 19:22:35
Job time: 8.93902 secs
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                                                                                                               biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 478;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 52.5; DB
; Pred. No. 54;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human diagnostic protein #21024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346 RNDNNGYGPPGG-HGHLMAGNP 366
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45.5%;
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9US-01609B1
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99US-0162142
                                                       9US-0158029
                           90S-0157865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 45.59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT, Liu C,
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N-PSDB; AAS85220.
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0.5 - 0.2 - 1.999, 0.6 - 0.2 - 1.999, 0.6 - 0.2 - 1.999, 0.6 - 0.2 - 1.999, 0.6 - 0.2 - 1.999, 0.6 - 0.2 - 1.999, 0.6 - 0.2 - 1.999, 0.6 - 0.2 - 1.999, 0.6 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 - 0.2 
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TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
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PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence b, Application US, Patent No. US20020106742A1 GENERAL INFORMATION:
                                                                                                                                                                                June 3, 2003, 19:24:01; Search time 51.565 Seconds (without alignments) 422.051 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                       1122
1 MDYQVSSPIYDINYTTSEPC......AACHGHLLLGNPKNSASVSK 215
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1. /cgn2_6/ptodata/1/pubpaa/USGB_NEW_PUB.pep:*
2. /cgn2_6/ptodata/1/pubpaa/USGB_NEW_PUB.pep:*
3. /cgn2_6/ptodata/1/pubpaa/USGG_NEW_PUB.pep:*
4. /cgn2_6/ptodata/1/pubpaa/USG_PUBCOMB.pep:*
5. /cgn2_6/ptodata/1/pubpaa/USG_NEW_PUB.pep:*
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13. /cgn2_6/ptodata/1/pubpaa/USGB_PUBCOMB.pep:*
14. /cgn2_6/ptodata/1/pubpaa/USGB_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             383519 seqs, 101223694 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                         - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                          US-09-938-703-6
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                                                                                                                                                                                                                                                                                                             Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ADDRESSEE: Knobbe, Martens, Olson & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach

NUMBER OF SEQUENCES: 17 CORRESPONDENCE ADDRESS:

COMPUTER READABLE FORM:

STATE: CA COUNTRY: U.S.A.

Sequence 6, Appli Sequence 6, Appli Sequence 4, Appli Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Description 0 US-09-938-719-6 0 US-09-938-719-6 0 US-09-938-703-6 0 US-09-938-703-4 0 US-09-938-703-4 0 US-09-938-703-4 0 US-09-938-703-4 0 US-09-734-221A-14 0 US-09-734-221A-14 0 US-09-759-818-2 0 US-09-759-818-2 0 US-09-759-818-2 0 US-09-759-818-2 0 US-09-759-818-2 0 US-09-756-818-2 0 US-09-756-818-2 0 US-09-756-818-2 0 US-09-756-818-2 0 US-09-756-818-2 0 US-09-796-202-1 22222222 01 01 0 6 6 6 Query Match Length 1000.0 10000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1 1122 1122 1958 9958 9958 9958 9958 9958 Score No. Result

MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,719
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 27-YULY-2000
ATTORNEY/AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: <Unknown>

NAME: Altman, Daniel E REGISTRATION NUMBER: 34,115

TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 6:

LENGIH: 215 amino acids SEQUENCE CHARACTERISTICS: INFORMATION FOR SEQ ID NO: 6:

TYPE: amino acid

20	958	85.4 85.4	352	200	-09-938-703 -09-502-783	v, v, v
22	926	84.4	352	70	US-10-106-623-2 US-09-813-653-17	Sequence 2, Appli Sequence 17, Appl
24	943	84.0	352	10	US-09-779-879A-2	(7)
25	943	84.0	352	10	US-09-779-880A-2	'n
26	933	83.2	352	17	US-10-106-623-20	ā
27	695	61.9	360	10	US-09-131-827A-20	
28	694	61.9	344		US-10-232-686-9	á
29	694	61.9	344		US-09-779-879A-9	5
30	694	61.9	344		US-09-779-880A-9	6
31	694	61.9	347	2	US-09-104-792-3	ń
32	694	61.9	360		US-09-131-827A-2	'n
33	692	61.7	360		US-09-938-719-7	,
34	692	61.7	360	10	US-09-939-226-7	Sequence 7, Appli
35	692	61.7	360		US-09-938-703-7	7
36	608.5	54.2	329		US-09-725-285-9	6
37	608.5	54.2	329		US-09-195-662A-9	6
38	608.5	54.2	329	10	US-09-339-912A-9	6
39	608.5	54.2	329	10	US-09-502-783A-9	6
40	598	53.3	355	10		Sequence 1, Appli
41	598	3	355	10	US-09-960-547-1	'n
42	598	53.3	375	σ	US-10-219-834-78	
43	594	52.9	355	10	US-09-938-719-9	
44	594		355	10	US-09-939-226-9	σì
45	294	52.9	355	10	US-09-938-703-9	Sequence 9, Appli
					ALIGNMENTS	
RESULT 1 US-09-93	RESULT 1 US-09-938-719-6					
; Sequence	nce 6, A	6, Application US/09938719	on US/	660	18719	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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                                                               61 IKSMIDIYLLNLAISDLFFILITVPFWAHYAAAQWDFGNIWCQLLIGLYFIGFFSGIFFII 120
                                                                                                                 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                         61 LKSMTDIYLLNLAISDLFFILTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; DB 10;
4.2e-104;
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                                                                                                                                                                                        181 HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215
                                                                                                                                                                                                              181 HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: INF. TEPT. COMPUTER: COMPUTER: INF. TEPT. COMPUTER: INF. TO-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Ver CURRENT APPLICATION DATA:

FILING DATE: 24 Aug-2001
CLASSIFICATION: CIRKDATON PATE: CLASSIFICATION CONFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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Pred. No. 4
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                 PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
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                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/09938703 Patent No. US202010870A1 GENERAL INFORMATION: APPLICANT: SAMSON, MICHEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2000-07-2 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08;
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Best Local Similarity 100.0
Matches 215, Conservative
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                                                                                                                                                                                                              121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                                                                                                                                                                                                                                          LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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                                                                                                                                   1 MDYQVSSPIXDINYXTSEPCQXINVKQIAARLLPPLYSLVFIFGFVGNMLVILLLINCKR 60
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: TBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pattentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: <u >CURNOWD></u>
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                                       Length 215;
                                                                           Indels
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ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                 Score 1122; DB 10;
Pred. No. 4.2e-104;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                             181 HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215
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INFORMATION FOR SEQ ID NO: 6:
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APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09939226 Patent No. US20020110805A1 GENERAL INFORMATION:
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                                     100.0%;
100.0%;
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                                                                         Conservative
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                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                     Best Local Sim:
Matches 215;
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JS-09-938-719-6
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US-09-939-226-4
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                                                                                                                                                                                                                         APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: AND INACTIVE CC-CHEMOXINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 IKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,719
FILING DATE: 24-Aug-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 27-JULY-2000
ATTORNEY AGENT INPORANTION:
NAME: ALITHAR, DANIEL E
REGISTRATION NUMBER: 34,115
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ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
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100.0%; Pred. No. 7.5e-88;
tive 0; Mismatches 0;
                                                       181 HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215
                                 HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-938-719-4
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Patent No. US20020106742al
GENERAL INFORMATION:
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Matches 184; Conservative
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HFPY 184
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                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
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ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 958; DB 10;
Pred. No. 7.5e-88;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: <UNKNOWD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: Intear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-939-226-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 09/626,939 FILING DATE: 2000-07-27
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100.08; Pre
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                                                                                   PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
Sequence 4, Application US/09939226 Patent No. US20020110805A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Altman, Daniel E
REGISTRATION NUMBER: 34
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                                                                 APPLICANT: SAMSON, MICHEL
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                                                                                                                                                                                                                                                                                      CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
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                                                                                                                                                                                              NUMBER OF SEQUENCES
                                                                                                                                                                                                                                                                                                        STATE: CA
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HFPY 184
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Gaps

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0; Indels

Length 352;

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61 LKSMIDIYLLNIAISDLFFLLTVPFWAHYAAAQWDFGNIMCQLLIGLYFIGFFSGIFFII 120
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                                                                                                                                                                                                                                                                                        61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLIGLYFIGFFSGIFFII 120
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; Publication No. US20030092632A1
; GENERAL INFORMATION:
    APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, Milliam C.
; TILLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 61010-AB-1
                                                                                                                                             Ouery Match 85.4%; Score 958; DB 9; I
Best Local Similarity 100.0%; Pred. No. 1.6e-87;
Matches 184; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/086,814
CURRENT FILING DATE: 2002-02-28
NUMBER OF SEQ ID NOS: 38
SOTWARE: Patentin version 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-734-221A-14; Sequence 14, Application US/09734221A; Publication No. US20030096221A1
   NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                           ; ORGANISM: Homo sapiens
US-10-232-686-2
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HFPY 184
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HFPY 184
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                                                       LENGIH: 352
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US-10-086-814-1
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                                                                            TYPE: PRT
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TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/10232686
Publication No. US20030023044A1
GENEBAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Li, Yi
CURRENT ELLIE OF INTENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10
FILE REPERBNCE: 1488.115.000
CURRENT FILIAG DATE: 2002-09-03
PRIOR APPLICATION NUMBER: 09/139,912
PRIOR APPLICATION NUMBER: 09/195,662
PRIOR PILING DATE: 1999-06-25
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 09/196,662
PRIOR APPLICATION NUMBER: 09/196,662
PRIOR APPLICATION NUMBER: 09/196,662
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 08/466,343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: Innear; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-09-938-703-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 184 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                           CITY: Newport Beach
                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 184; Conservative
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HFPY 184
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                                                                                                                                               COUNTRY:
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Length 352;

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APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10
TITLE OF INVENTION: CCRS Receptor)
TITLE OF INVENTION: (CCRS Receptor)
FILE REPERBACE: 1488.115003
CURRENT PILLING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 09/339,912
PRIOR RELING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-11-18
PRIOR FILING DATE: 1998-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LKSWTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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Best Local Similarity 100.0%; Pred. No. 1.6e-87;
Matches 184; Conservative 0; Mismatches 0;
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05-09-725-285-2
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Patent No. US20010039026A1
GENERAL INFORMATION:
APPLICANT: Rickett, Graham A
APPLICANT: Dobbs, Susan
APPLICANT: Perros, Manoussos
TITLE OF INVENTION: Assay Wethod
FILE REFERRACE: POLO348APME
CURRENT APPLICATION NUMBER: US/09/759,841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: GB 0000661.9
PRIOR PLING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: GB 0000661.9
PRIOR PLING DATE: 2000-01-12
PRIOR PLING DATE: 2000-01-12
PRIOR PLING DATE: 2000-01-12
PRIOR PLING DATE: 2000-01-12
NUMBER: GB 0000659.3
NUMBER: CB 0000659.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-01-12
3: 6
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                                      ; Sequence 2, Application US/09725285; Patent No. US2001000241A1
; GENERAL INFORMATION:
; APPLICAMT: Li, Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
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LENGIH: 352
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US-09-759-841-2
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                                                                                                                           TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                      ADDRESSEE: David A. Jackson, Esq. STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
REDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 11-Pec-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 352;
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APPLICATION NUMBER: US 08/666,020
FILING DATE: 19-JUN-1996
APPLICATION NUMBER: US 08/227,319
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-004 NZ
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487.5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 85.4%; Score 958; DB 9; I Best Local Similarity 100.0%; Pred. No. 1.6e-87; Matches 184; Conservative 0; Mismatches 0;
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SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-734-221A-14
                                                                                                                                                                         USES THEREOF
GENERAL INFORMATION:
APPLICANT: LITTANN, DAN R.
DENG, HONGKUI
ELLMEIER, WILERIED
LANDAU, NATHANIEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 352 amino acids
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                         STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                    CITY: Hackensack
                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                           LIU, RONG
                                                                                                                                                                                                                                                                                     Floor
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HFPY 184
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                                                                                                                                                                                                                                                                                                                                      61 LKSWTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                                                                                                                                                                        LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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                                                                                                                                     1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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APPLICANT: Rosehke, Viktor
APPLICANT: Rosehke, Viktor
APPLICANT: Rosehke, Viktor
APPLICANT: Rosehke, Viktor
APPLICANT: Ruben, M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
FILE REFERENCE: 1488.11500A
CURRENT APPLICATION NUMBER: US/09/779,879A
CURRENT FILING DATE: 2000-10-09
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 2000-03-09
                                                                                          Gaps
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                                          85.4%; Score 958; DB 10; Length 352; 100.0%; Pred. No. 1.6e-87; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22, Application US/09779879A Patent No. US20020048786Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 184; Conservative
                                                                  Best_Local Similarity 100.0
Matches 184; Conservative
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US-09-779-880A-22
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US-09-759-841-2
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APPLICANT: See, Raymond
APPLICANT: Tan Hehir, Christina
APPLICANT: Tan Hehir, Christina
APPLICANT: Tan Hehir, Christina
APPLICANT: Tan Hehir, Christina
TILE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compound
FILE REFRENCE: CNS-005
CURRENT FILING DATE: 2000-03-20
FRIOR APPLICATION NUMBER: US 60/190,946
PRIOR FILING DATE: 2000-03-21
FRIOR PALICATION NUMBER: US 60/190,996
PRIOR FILING DATE: 2000-03-21
PRIOR PLICATION NUMBER: US 60/191,299
PRIOR PLICATION NUMBER: US 60/191,299
PRIOR PLICATION NUMBER: US 60/191,299
PRIOR PLICATION NUMBER: 300-03-21
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PAtentin version 3.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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                                                                          APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Rosenke, Viktor
APPLICANT: Rosenke, Viktor
APPLICANT: Ruben, Steven, M.
TILLE APPLICANT: Ruben, Steven, M.
TILLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNRIO
FILE REPERENCE: 1488 115000C
CURRENT APPLICATION NUMBER: US/09/779,880A
CURRENT FILING DATE: 2000-02-09
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 58
SOGTWARR: Patentin version 3.0
SEQ ID NO 22
TENANTH: 34.2
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Sequence 22, Application US/09779880A Patent No. US20020061834A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15, Application US/09813653
Patent No. US20200064770Al
GENERAL INFORMATION:
APPLICANT: Nestor, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson, Carol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-779-880A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRGANISM: Homo sapiens
US-09-813-653-15
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HFPY 184
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US-09-813-653-15
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                                                                                                                                                          61 LKSMTDIYLLNLAISDLFFELLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
                                                                                    61 LKSMTDIYLLINLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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                                                                     1 MDYQVSSPIYDINYYISEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/09796202
; Patent No. US2020066813A1
; GRUREAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Dasor, William
; TITLE OF INVENTION: SULFATED CR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REPERENCE: 2048/61010/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; UNDRENT PILING DATE: 2001-02-28
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 17
; LEMPERED FOR SEQ ID NOS: 17
; LEMPERED FOR SEQ ID NOS: 17
; LEMPERED FOR SEQ ID NOS: 17
                                   0;
Query Match 85.4%; Score 958; DB 10; Length 352; Best Local Similarity 100.0%; Pred. No. 1.6e-87; Matches 184; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.6e-87;
Matches 184; Conservative 0; Mismatches 0;
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HFPY 184
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181 HFPY 184
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ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
JS-09-796-202-1
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June 3, 2003, 19:21:31 ; Search time 4.53659 Seconds (without alignments) 201.057 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/BCCOMB.pep:*
6: /cgn2_6/ptodata/1/iaa/pcruS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                              1 IKDSHLGAGPAAACHGHLLLGNPKNSASVSK 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                               262574 seqs, 29422922 residues
                                                                                                                                                                                                                                          US-09-938-703-6_COPY_185_215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                       protein ~ protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
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                                                                                                                                                           Run on:
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Description \$ Query Match Length DB

SUMMARIES

Sequence 13, Appl Sequence 17, Appl Sequence 6, Appli Sequence 13, Appl Sequence 4, Appli 6, Appli 28, Appl 6, Appli Sequence 8, A Sequence 6, A Sequence 6, A Sequence 6, A Sequence 28, A Sequence 1, A Sequence 2, A S Sequence 2, A Sequence 3, A Se US-09-833-752-6
US-08-640-963-13
US-08-612-133A-8
US-08-712-133A-8
US-08-717-6
US-09-037-601-6
US-09-037-601-6
US-09-209-916-1
US-09-209-916-1
US-08-813-813B-3
US-08-813-813B-3
US-08-813-813B-3
US-08-813-813B-3
US-08-813-813B-3
US-08-813-813B-3
US-08-813-813B-3
US-09-816-1
US-09-813-813B-3
US-09-813-813B-3
US-09-813-813-2
US-09-813-813-2
US-07-814-0818-4
US-08-251-937A-4
US-08-251-133A-2
US-08-251-133A-3
US-08-251-133A-3
US-08-251-133A-4
US-08-251-133A-4
US-08-251-133A-3
US-08-251-133A-3 US-08-670-707A-2 US-09-037-601-2 US-09-324-867-3 US-09-315-179-2 1438 1661 1661 1661 1661 1958 Result Š

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Gaps ; 0

Length 34; Indels

Query Match 100.0%; Score 164; DB 4; Best Local Similarity 100.0%; Pred. No. 8.9e-18; Matches 31; Conservative 0; Mismatches 0;

1 IKDSHLGAGPAAACHGHLLLGNPKNSASVSK 31

ŏ g RESULT 2

Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Patent No. 5171844 Patent No. 5171844 Patent No. 5171846 Sequence 27, Appl Sequence 27, Appl Sequence 22, Appli Sequence 25, Appli Sequence 3, Appli		MCODING SAID RECEPTOR (EPO)
US-09-523-656-2 PCT-US93-03275-4 PCT-US94-13200-2 US-08-131-202-2 US-08-13-1202-2 15-1744-2 15-42260-1 US-09-177-165A-27 US-09-177-165A-24 US-09-177-165A-24 US-09-177-119-3 US-09-091-219-2 US-09-091-219-2 US-09-091-219-3 US-09-34-613-8 US-08-543-084A-32 US-09-543-084A-33	ALIGNMENTS	ICHEL REDERICK REDERICK AND INACTIVE CC-CHEMOKINES R. AND NUCLEIC ACID MOLECULES ENCODING 17 Martens, Olson & Bear 17 Martens, Olson & Leth Floor 18 Martens, Olson & Leth Floor 19 Martens, Olson & Leth Floor 10 Martens, Olson & Leth Floor 10 Martens, Olson & Leth Floor 11 Martens, Olson & Leth Floor 12 Martens, Olson & Leth Floor 13 Martens, Olson & Leth Floor 15 Martens, Olson & Leth Floor 16 Martens, Olson & Leth Floor 17 Martens, Olson & Leth Floor 18 Martens, Olson & Leth Floor 18 Martens, Olson & Leth Floor 19 Martens, Olson & Leth Floor 10 Martens, Olson & Leth Floor 11 Martens, Olson & Leth Floor 12 Martens, Olson & Leth Floor 13 Martens, Olson & Leth Floor 14 Martens, Olson & Leth Floor 17 Martens, Olson & Leth Floor 18 Marten
27.7 2332 5 2332 5 27.7 23332 5 23332 5 23332 5 23332 5 23332 6 23351 1 22351 1 2235 4 2251 1 2235 4 2256 8 1188 2 256 8 1188 2 256 8 256		ion ion ion ion ion ion ion ion
29 30 30 30 31 31 31 32 33 33 34 44 55 44 55 44 56 44 56 44 57 47 57 47 57 47 57 57 57 57 57 57 57 57 57 57 57 57 57		RESULT 1 US-08-833-752-13 US-08-833-752-13 Sequence 13, Application Patent No. 644837 PAPLICANT: SAMSON, APPLICANT: PARKINITIN APPLICANT: LIBERT, ITILE OF INVENTION: TITLE OF INVENTION: TOWNERS OF SEQUENCES: CORPUTER: CA COUNTRY: U.S.A. ZIP: 92660 COMPUTER: IBM PC OPERATING SYSTEM: MEDIUM TYPE: Flopy COMPUTER: IBM PC OPERATION SYSTEM: SOFTWARE: PATENTION APPLICATION UNMERRED FILING DATE: 9-APP CLASSIFICATION: 53 ATTORNER/AGENT INFORM REFERENCE/POCKET IN INFORMATION FOR SEQ ID SEQUENCE CHARACTERIS: LENGTH: 34 amino acid STRANDEDNESS: sin TYPE: amino acid STRANDEDNESS: sin TOPOLOGY: linear
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APPLICANT: Thorner, Michael O.
APPLICANT: Gaylinn, Bruce D.
APPLICANT: Gaylinn, Bruce D.
APPLICANT: Gaylinn, Brice D.
APPLICANT: Lyons Yr., Charles E.
TITLE OF INVENTION: MOLECULAR CLONING OF THE OVINE PITUITARY
TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE RECEPTOR
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: POPHAM, HAIK, SCHNOBRICH & KAUFMAN, LTD.
STREET: Metropolitan Square Building, Suite 800, 1450
STREET: G. Street
CITY: Mashington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 164; DB 4; Length 215; 100.0%; Pred. No. 7.6e-17; Live 0; Mismatches 0; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEZ/ASENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: 34,115
REFERENCE/DOCKET NUMBER: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acids
TYPE: amino acids
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APPLICATION NUMBER: US/08/660,963
FILING DATE: 12-UN-1996
FILING DATE: 12-UN-1996
ATTORNEY/AGENT INFORMATION:
NAME: O'Shaughnessy, Brian P.
REGISTRATION UNDERS: 32,747
REGISTRATION UNDERS: 32,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 IKDSHLGAGPAAACHGHLLIGNPKNSASVSK 215
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WEDLOW TYPE: Floppy disk
COMPUTER: TIM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/08660963
Patent No. 5852187
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-824-8000
TELEFAX: 202-824-8199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELERA: 202-824-8199
TELEX: 248516
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 100.
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                               US-08-833-752-6
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Sequence 17, Application US/09087232A
Patent No. 6153431
GENERAL INFORMATION:
APPLICANT: QUILLENT GUILLENT GUILLENT TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
STREET: 30 Rockefeller Plaza
CIT: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08833752
Fatent No. 6448375
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: PARMENTIER, MARC
APPLICANT: LIBERT
APPLICANT: APPLICANT: REDERICK
ITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES:
ADDRESSER: Knobbe, Martens, Olson & Bear
STREET: 6CO Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
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                                                                                                                                                                                                                                                                                                                                                                    COUNTY TOTAL
COMPUTER INTERACE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: INDE PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOTUMARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/08/,232A
FILING DATE: 28 MAY 1998
CLASSIFCATION DATA:
APPLICATION NUMBER: 60/048,057
FILING DATE: 30 MAY 1997
ATTORNEY/AGENT INFORMATION:
NAME: KOLE, LISA B.
REGISTRALION NUMBER: 35,225
REGISTRALION NUMBER: 35,225
REGISTRALION NUMBER: 35,225
REGISTRALION NUMBER: 35,225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: AP 31115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2628
TELEPRAX: (212) 765-2519
INFORMATION POS SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 anino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-833-752-6
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NAME: Pratt, John S.
REGISTRATION NUMBER: 29,476
REFERENCE/DOCKET NUMBER: EM
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TELEPHONE: 404-815-6500
TELEPAT. 404-815-6555
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.0%;
40.0%;
                                                                                                                                                               LENGIH: 2319 amino acids
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                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mus musculus PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 40.0
Matches 12; Conservative
                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL: Genomics
VOLUME: 16
                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374-379
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30309
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                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-474-503-6
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APPLICANT: Cameron, Cherie
APPLICANT: Cameron, Cherie
APPLICANT: Horrocks, L. Suzanne Hoyle
APPLICANT: Horrocks, L. Suzanne Hoyle
APPLICANT: Horrocks, L. Suzanne Hoyle
TILLE APPLICANT: Hough, Christine
FILE REPERENCE: 1669.0010002/JAG/BDD
CURRENT APPLICATION NUMBER: US/09/324,867A
CURRENT PILING DATE: 1999-06-03
EARLIER APPLICATION NUMBER: 09/035,141
EARLIER PILING DATE: 1999-06-03
EARLIER PILING DATE: 1999-06-03
EARLIER PILING DATE: 1999-06-03
EARLIER PILING DATE: 1997-03-06
MUMBER FO END DATE: 1997-03-06
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                                           Gaps
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Score 50; DB 2; Length 501;
Pred. No. 17;
8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LOLlar, John S.
APPLICANT: Lollar, John S.
APPLICANT: Runge, Marschall S.
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: March 11, 1994
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Pred. No. 2.3e+02;
3; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KDSHLG-AGPAACHGHLLLGNPKNSASVS 30
                                                                                                     |:|| |: | || |: || 473 SYLGLPPSTASHGSLML--PPSTSFLSR 498
                                                                                4 SHLGAGPAAACHGHLLLGNPKNSASVSK 31
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PRIOR APPLICATION DATA:
PPLICATION NUMBER: US 07/864,004
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                     Sequence 4, Application US/09324867A Patent No. 6251632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08212133A Patent No. 5663060 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Kilpatrick & Cody STREET: 100 Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.0%;
40.0%;
    30.5%;
39.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 2304
    Query Match
Best Local Similarity 39.33
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-324-867-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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US-08-212-133A-8
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STATE:
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Score 47.5; DB 1; Length 2319;
Pred. No. 2.3e+02;
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APPLICANT: EMOCY University
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DATE: 1993
RELEVANT RESIDUES IN SEQ ID NO: 8: FROM 1 TO 2319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION NOTHER: 05/08/474,503
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS: Lakich, D.
AUTHORS: Gitschier, J.
TILLE: Sequence of the Murine Factor VIII cDNA.
Patent No. 5663060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .... AUURESS:
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
COUNTRY: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KDSHLG-AGPAAACHGHLLLGNPKNSASVS 30
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: EMU/76677
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-572-6508
TELEPRAX: 404-572-6555
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 6, Application US/08474503
; Patent No. 5744446
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REFERENCE/DOCKET NUMBER: 75
ELECOMMUNICATION INFORMATION:
                                                                                                                                                         FRAGMENT TYPE: N-terminal SOUTGINE, SOURCE: ORGANISM: Mus muscrilus PUBLICATION INFORMATION: AUTHORS: Lakich, D. AUTHORS: Gitschier, J. AUTHORS: Gitschier, J.
  SEQUENCE CHARACTERISTICS:
LENGTH: 2319 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 303/499-8080
TELEFAX: 303/499-8089
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Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSE: Greenlee, V
STREET: 5370 Manhattar
CITY: Boulder
                                                                                                 MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
                                                           STRANDEDNESS: single
                                           amino acid
                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Colorado
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lollar, John S.
TITLE OF INTENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                              6: FROM 1 TO 2319
                                                                                                                                                                         ORGANISM: Mus musculus
PUBLICATION INFORMATION:
AUTHORS: Elder, F.
AUTHORS: Lakich, D.
AUTHORS: Gitschier, J.
TITLE: Sequence of the Murine Factor VIII CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Greenlee, Winner and Sullivan, P.C. STREET: 5370 Manhattan Circle Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US94/13200
FILING DATE: 15-NOV-1934
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,133
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KDSHLG-AGPAAACHGHLLLGNPKNSASVS 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/670,707A
FILING DATE: 26-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/864,004
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Greenlee, Lorance L.
REGISTRATION NUMBER: 27,894
REFERENCE/DOCKET NUMBER: 75-95F
TELECOMMUNICATION INFORMATION:
TELECPHONE: 303/499-8080
TELEFRAX: 303/499-8089
                                                                                                                                                                                                                                                                                                                                                                                            RELEVANT RESIDUES IN SEQ ID NO: US-08-474-503-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08670707A Patent No. 5859204 GENERAL INFORMATION:
                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HPOTHERICAL: YES
ANTI-SENSE: NO
FRACMENT TYPE: N-terminal
ORIGINAL SOURCE:
2319 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 303/499-808
TELEFAX: 303/499-8089
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 40.0
Matches 12; Conservative
                                         single
                                                                                                                                                                                                                                                                                                                    Genomics
                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                       374-379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boulder
STATE: Colorad
                    TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                           Patent No. 5744446
JOURNAL: Genc
                                                                                                                                                                                                                                                                                                                                  VOLUME: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 80303
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Gaps
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Patent No. 6180371
GENERAL INFORMATION:
APPLICANT: Lollar, John S.
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 40
                                                                        ; PAGES: 374-379
; DATE: 1993
; RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 1 TO 2319
US-08-670-707A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: ILIN FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,601
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
TITLE: Sequence of the Murine Factor VIII cDNA
Patent No. 5859204
JOURNAL: Genomics
VOLUME: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Greenlee, Winner and Sullivan, P.C. 5370 Manhattan Circle Suite 201
                                                                                                                                                                                                                                                                                                                                   1832 RDMHSGLIGPLLICHANTL--NPAHGRQVS 1859
                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: WO PCT/US94/13200 FILING DATE: 15-NOV-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/212,133 FILING DATE: 11-MAR-1994 PRIOR APPLICATION NUMBER: US 07/864,004
                                                                                                                                                                                                                                                                                                   2 KDSHLG-AGPAAACHGHLLLGNPKNSASVS 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 07-APR-1992
ATTORNEY/AGBNT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION WITHOUT
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Indels
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TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PEC-DOS/MS-DOS
SOFTWARE: PEC-DOS/MS-DOS
SOFTWARE: PECEDIN Release #1.0, Version #1.25
APPLICATION NUMBER: PCT/US94/13200
FILING DATE: 15-NOV-1994
CLASSIPICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47.5; DB 4;
Pred. No. 2.3e+02;
3; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1832 RDMHSGLIGPLLICHANTL--NPAHGRQVS 1859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: EMU106CIP(2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-815-6598
INFORMATION FOR SEG ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2319 amino acids
                                                                                                                               APPLICANT: Lollar S., John
TITLE OF INVENTION: MODIFIED FACTOR VIII
FILE REFERENCE: 75-951
CURRENT APPLICATION NUMBER: US/09/523,656
CURRENT FILING DATE: 2000-03-10
EARLIER FILING DATE: 1998-03-10
EARLIER APPLICATION NUMBER: 09/037,601
EARLIER APPLICATION NUMBER: 08/070,707
EARLIER FILING DATE: 1996-06-26
NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KDSHLG-AGPAAACHGHLLLGNPKNSASVS 30
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                                                          ; Sequence 28, Application US/09523656
; Patent No. 6458563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 29.0%;
Best Local Similarity 40.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 2319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mus musculus
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TOPOLOGY: linea.
MOLECULE TYPE: protein
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Mus musculus
US-09-523-656-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Atlanta
STATE: Georgia
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Georgia
                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 30309
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                               JS-09-523-656-28
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                                                                                                                                                                                                                                                                                                                               AUTHORS: Elder, F.
AUTHORS: Lakich, D.
AUTHORS: Gitschier, J.
TITLE: Sequence of the Murine Factor VIII cDNA
Patent No. 6180371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 29.0%; Score 47.5; DB 4; Best Local Similarity 40.0%; Pred, No. 2.3e+02; Matches 12; Conservative 3; Mismatches 12;
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CURRENT FILING DATE: 1999-05-20
EARLIER APPLICATION NUMBER: U.S. 09/037,601
EARLIER FILING DATE: 1998-03-10
EARLIER FILING DATE: 1996-06-26
EARLIER FILING DATE: 1996-06-26
EARLIER APPLICATION NUMBER: PCT/US97/11155
EARLIER APPLICATION NUMBER: PCT/US97/11155
EARLIER FILING DATE: 1994-11-15
EARLIER FILING DATE: 1994-11-15
EARLIER FILING DATE: 1994-11-15
EARLIER FILING DATE: 1994-03-11
EARLIER FILING DATE: 1994-03-11
EARLIER FILING DATE: 1994-03-11
EARLIER FILING DATE: 1994-03-11
EARLIER FILING DATE: 1998-03-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LOILST, John S
TITLE OF INVENTION: Modified Factor VIII
FILE REFERENCE: 75-95H
CURRENT APPLICATION NUMBER: US/09/315,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09315179
Patent No. 6376463
GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 2319 amino acids TYPE: amino acid STRANDEDNESS: aingle TOPOLOGY: linear
                                                                                                                                                                                                                          FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                  ORGANISM: Mus musculus PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Conservative
                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Mus musculus
US-09-315-179-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAGES: 374-379
DATE: 1993
                                                                                                                                                                             HYPOTHETICAL: YI ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DS-09-037-601-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
US-09-315-179-6
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Best Local S
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Matches
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Remillard, Janoe E.
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: TTI-
TELEPHONE: (617,227-400
TELEPHONE: (617)227-5941
: INFORMATION FOR SED ID NO: 3:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-882-083-2
; Sequence 2, Application US/0882083
; Patent No. 5869292
; Patent INFORMATION:
; APPLICANT: VOORBERG, Johannes J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1661 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 1471 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-683-839B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3000 K St
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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IIII. Charles . R. et al.
IIIIE OF INVENTION: Use of Viral Cis-Acting Post-Transcriptional
IIIIE OF INVENTION: Regulatory Sequences To Increase Expression of
IIIIE OF INVENTION: Intronless Genes Containing Near-Consensus Splice Sites
CORRESPONDENCE ADDRESS: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Derived from ; OTHER INFORMATION: human factor VIII sequence US-09-209-916-1
                                                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                             Length 2319;
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Pred. No. 2.6e+02;
3; Mismatches 12; Indels 3
                                                                                                                                                                                                                                                                                     12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/0920916
Fatent No. 6358703
GENERAL INFORMATION:
APPLICANT: Cho., Myung-Sam
APPLICANT: Cho., Myung-Sam
TILE OF INVENTION:
FILE REFERENCE: MSB-7255
CURRENT APPLICATION NUMBER: US/09/209,916
CURRENT APPLICATION NUMBER: US/09/209,916
CURRENT APPLICATION NUMBER: US/09/209,916
CURRENT APPLICATION NUMBER: US/09/209,916
SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO: 1438
LENGTH: 1438
                                                                                                                                                                                  6: FROM 1 TO 2319
                     : Elder, F.
: Lakich, D.
: Gitschier, J.
Sequence of the Murine Factor VIII cDNA.
: Genomics
                                                                                                                                                                                                                                         Score 47.5; DB 5;
Pred. No. 2.3e+02;
3; Mismatches 12;
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                                                                                                                                                                                                                                                                                                                      2 KDSHLG-AGPAAACHGHLLLGNPKNSASVS 30
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STREET: 60 State Street, suite 510
                                                                                                                                                                                ; RELEVANT RESIDUES IN SEQ ID NO: PCT-US94-13200-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08683839B Patent No. 5744326
GENERAL INFORMATION:
                                                                                                                                                                                                                                         29.0%;
40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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Best Local Similarity 40.0%;
Matches 12; Conservative
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                                                                                                                                                                                                                                                          Local Similarity 40.0 hes 12; Conservative
UBLICATION INFORMATION:
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                                                                                                                                        374-379
1993
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US-08-683-839B-3
                                                                                                  JOURNAL:
                                       AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
JS-09-209-916-1
                                                               AUTHORS:
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                                                                                                                       VOLUME:
                                                                                                                                        PAGES:
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                                                                               TITLE:
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Matches
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VOORBERG, Johannes J.
WENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY
SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patcharin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,839B
FILING DATE: 11-MARCH-1996
CLASSIFICATION A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              984 KDVHSGLIGPLLVCHTNTL--NPAHGRQVT 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08 08/558,107
FILING DATE: 13-NOV-1995
ATTONEY/AGENT INFORMATION:
NAME: ISACSOM, John P.
REGISTRATION NUMBER: 33,715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30472/212
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Scoring table:

Searched:

Perfect score:

Sequence:

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Run on:

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Sequence 13, Application US/09087232A
Patent No. 6153431
GENERAL INFORMATION:
APPLICANT: Quillent et al.
TITLE OF INVENTION: HOMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
NUMBER OF SEQUENCES: 23
CORRESPONDENCE S. 23
ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
STREET: 30 Rockefeller Plaza
                                                              Sequence 2, Appil Sequence 2, Appil Sequence 2, Appil Sequence 9, Appil Sequence 17, Appil Sequence 5, Appil Sequence 5, Appil Sequence 5, Appil Sequence 5, Appil Sequence 6, Appil Sequence 6, Appil Sequence 6, Appil Sequence 5, Appil Sequence 53, Appil
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MEDLIN TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                              US-08-466-343D-9
US-09-087-232A-17
US-08-833-752-6
US-08-012-988A-5
US-08-450-393A-5
US-09-239-938-1
PCT-US95-00476-5
                                                                                                                                                                                   US-08-833-752-9
US-08-833-752-4
US-09-534-185-53
US-08-575-967A-4
US-08-575-967A-4
US-08-575-967A-4
US-09-634-185-54
US-09-534-185-54
US-09-232-878-2
US-09-634-185-55
US-09-634-185-55
                                         US-09-045-583-51
US-09-534-185-51
US-08-450-393A-2
                                                                                    PCT-US95-00476-2
                     PCT-US95-00476-4
                                US-08-833-752-7
                                                                           US-08-446-669-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/087,232A FILING DATE: 28 MAY 1998 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,057
FILING DATE: 30 MAY 1997
ATTONNEY-AGENT INFORMATION:
NAME: KOLE, LISA B.
REGISTRATION NUMBER: 35,225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 408-2628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 765-2519
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
STREET: 30 Rockef
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
RESULT 1
US-09-087-232A-13
                                                                         1191
1191
1190.5
1122
1003.5
1003.5
1003.5
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857.5
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2, Appli
5, Appli
52, Appl
52, Appl
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Sequence 14, Appl
                                                                                      (without alignments)
3063.973 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                           1 GAATTCCCCCAACAGAGCCA......AGTAGATTAGATCCGAATTC 1442
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Sequence 4,
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Sequence 2
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                                                                           3, 2003, 18:44:09 ; Search time 27.6947 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

    protein search, using frame_plus_n2p model

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US-08-575-967A-2
US-08-933-752-5
US-09-045-583-52
US-09-534-185-52
US-08-466-3430-2
US-08-461-244
US-08-461-2443
US-08-446-669-4
                                                                                                                                                                                                                                                        Potal number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                 262574 segs, 29422922 residues
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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                                                                                                                        US-09-938-703-3
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Match Length
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1745.5 1745.5 1745.5 1739.5 1730.5 1718.5 1463.5 1331 1331

264397

Score 1745.5

Result Š.

Database :

53, Appl 4, Appli 1, Appli

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1047 GGTGACAGACACTCTTGGGATGACGCACTGCTGCATCAACCCCATCATCTATGCCTTTGT 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/666,020
FILING DATE: 19-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION NUMBER: US 08/227,319
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1049-1-004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                           Séquence 14, Application US/08861105
Patent No. 6258527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Jackson Esq., David A. REGISTALION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 1045 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 352 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New State
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                 Indels:
                                                                                    5.68e-182
1745.50
96.60%
: 96.32%
66.42%
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
                                               MOLECULE TYPE: protein
                        amino acid
                                      linear
                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                           US-09-087-232A-13
                                                                                     Alignment Scores:
                                    TOPOLOGY:
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APPLICANT: LITMAN, DAN R.
APPLICANT: BELMAIRE, HONGKUI
APPLICANT: ELLMAIRE, WILFRIED
APPLICANT: LANDAU, NATHANIEL R.
APPLICANT: LANDAU, NATHANIEL R.
TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
TITLE OF INVENTION: MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                     1167 CIGCAAAIGCIGIICIAIITICCAGCAAGAGGCICCCGAGCGAGCAAGCICAGIIIACAC 1226
                                                               CGGGGAGAAGIICAGAAACIACCICITAGICITCIICCAAAAGCACAIIGCCAAACGCIT 1166
1227 CCGATCCACTGGGGAGCAGGAATATCTGTGGGCTTG 1263
                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 14
CORRESPONDENCE 114
CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza,
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.30
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300 CAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG 359
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                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Gray et al.
TITLE OF INVENTION: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                            Murray & Borun
Drive
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                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/575,967A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                           3: Marshall, O'Toole, Gerstein,
6300 Sears Tower, 233 S. Wacker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
                                                                                                                                     Sequence 2, Application US/08575967A Patent No. 6265184
                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: No. 6265184and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 32.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-485-1900
TELEFAX: 206-485-1662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 352 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature OTHER INFORMATION: /- '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
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Best Local Similarity:
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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                                                                                                                                                                                                                                                                       CTGAAGAGCATGACTGACCTGCTCGACCTGGCCATCTCTGACCTGTTTTCCTT
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             352
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          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                US-09-938-703-3 (1-1442) x US-08-861-105-14 (1-352)
          5.68e-182
1745.50
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                                              Best Local Similarity:
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Alignment Scores:
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                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
FILLING DATE: 9-ARR-1997
CLASSIFICATION: 536
ATTONIEY AGENT INFORMATION:
ATTONIEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
  SSEE: Knobbe, Martens, Olson & Bear
F: 620 Newport Center Drive 16th Floor
Newport Beach
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                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
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REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 5:
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96.60%
96.32%
66.42%
                                                                                                                                                                                                                                                                  : 352 amino acids
amino acid
                         CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE: FORM:
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                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-833-752-5
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Best Local Similarity:
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     ADDRESSEE:
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APPLICANT: SAMSON, MICHEL
APPLICANT: PARABRATISH, MARC
APPLICANT: PARABRATISH, MARC
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
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Patent No. 6448375
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338
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115
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                               1739.50
96.60%
95.75%
66.19%
               TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-045-583-52
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    amino acid
3Y: linear
                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                        Alignment Scores:
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                                                                            APPLICANT: Graham, Gerard J. et al.
IIILE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
                                                          CTTGGGGCTGGTCCTGCCTGCTTGTCATGGTCATCTGCTACTCGGGAATCCTAAAAAC
                                                                                                                  TCTGCTTCGGTGTCGAAATGAGAAGAAGAGGCACAGGGCTGTGAGGCTTATCTTCACCAT
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Ralease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Mandragouras, Any E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMUNICATION INFORMATION:
TELEBRAK: (617)227-7400
TELEFAR (617)227-7400
TELEFAR (617)227-7400
TELEFAR (617)227-7400
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 52, Application US/09045583 Patent No. 6287805
CATTITCCATAC-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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STATE: Massachusetts
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                       CIGAAGAGCATGACTGACTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT
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US-08-466-343D-2
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                                               240 AIGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATGGAGGCCCTGC 299
                                                                                                                                                                                                                          APPLICANT: Graham, Gerard J. et al.
IITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
ENT APPLICATION DATA:
FILING DATE: 24-Mar-2000
CLASSIFICATION: CURKNOWN>
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Mismatches:
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                                                                                                                                                                                                                                                                                              ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street
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Matches:
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FILING DATE: <UNKNOWN>
ATTORNET/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPRONE: (617)227-7400
TELEPRONE: (617)742-4214
INFORMATION FOR SEO ID NO: 52:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                           Sequence 52, Application US/09534185 Patent No. 6403767 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                     CITY: Boston
STATE: Massachusetts
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1739.50
96.60%
95.75%
66.19%
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CORRESPONDENCE ADDRESS:
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Best Local Similari
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Pred. No.:
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US-09-534-185-52
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APPLICANT: Kwon, Douglas S.
APPLICANT: Kwon, Douglas S.
APPLICANT: Genjuens S.
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
FILE REFERENCE: 1049-1-017
CURRENT APPLICATION NUMBER: US/09/517,605
CURRENT FILING PARE: 2000-03-02
NUMBER OF SEQ. ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
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Mismatches:
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Patent No. 6391567
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ORGANISM: Homo sapiens
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Best Local Similarity:
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LENGIH: 352
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                                                                                                            ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,343D
FILING DATE: 06-UNN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                      RAME: STEEFE, ERLC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.
TELECOMMUNICATION: TELEPHONE: (202) 371-2600
TELEPRX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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1730.50
96.32%
95.18%
65.85%
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amino acid
             GENERAL INFORMATION:
APPLICANT: LI, YI
TITLE OF INVENTION: CHEN
TITLE OF INVENTION: CHEN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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Best Local Similarity:
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                                                                        Sequence 2, Application US/08724984A
Patent No. 6388055
GENERAL INFORMATION:
APPLICANT: Derk Bergsma, Mary Brawner, and Usman Shabon
TITLE OF INVENTION: No. 638805551 Mouse Genomic Clone of the CC-TITLE OF INVENTION: CKR5 Receptor
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   1227 CCGATCCACTGGGGAGCAGGAATATCTGTGGGGCTTG 1263
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                 US-09-938-703-3 (1-1442) x US-08-724-984A-2 (1-354)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches:
Indels:
                                                                                                                                                                            ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road, P.O. Box 1539 CITY: King of Prussia
                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb
COMPUTER: IBM 486
                                                                                                                                                                                                                                                                                         WINDOWS FOR WORKGROUPS
)FI WORD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270 5024
TELEFAX: 610 270 5090
                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: William T. Han
REGISTRATION NUMBER: 34,34.
REFERENCE/DOCKET NUMBER: A
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1463.50
86.48%
78.59%
55.69%
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                                                                                                                                                                                                                                                                            COMPUTER: IBM 486
OPERATING SYSTEM: WIND
SOFTWARE: MICROSOFT WO
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                   NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity: 8
Best Local Similarity: Query Match: BB:
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US-08-724-984A-2
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COUNTRY:
ZIP: 1940
                                                                US-08-724-984A-2
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                                                                            PatentIn Release #1.0, Version #1.30
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Mismatches:
Indels:
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Matches:
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,244
FILING DATE: 05-001-1995
                                                                                                                                                                           NAME: Ferraro, Gregory D. REGISTRATION NUMBER: 36,134
                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 32:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                 9.81e-137
1331.00
83.76%
73.50%
50.65%
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                              CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                      LENGTH: 347 amino acids
                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                      TYPE: amino acid STRANDEDNESS:
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Best Local Similarity:
Query Match:
                                                                                                                                             CLASSIFICATION:
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101 IleMetCysLysValPheThrGlyValTyrHisIleGlyTyrPheGlyGlyIlePhePhe 120
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                                                                                                                                                                                             ATCATCCTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATGCTGTTTGCTTTAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08461244
Patent No. 5776729
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R.
APPLICANT: Yi, Li
APPLICANT: Ruben, Steven M.
APPLICANT: Rosen, Craig A.
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CORRESPONDENCE ADDRESS:
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COUNTRY: USA
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                                                                                                                                                                                                                               14 AsnGluSerGlyGluGluValThrThr---PhePheAspTyrAspTyr-----GlyAla
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                Gaps:
                                                                     9.96e-137
1331.00
83.76%
73.50%
50.65%
TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                Similarity:
                                                                                                Percent Similarity
                                                        Alignment Scores:
                           US-08-450-393A-4
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                                         GCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTCGGGAATCCTAAAAACTCTGCT
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APPLICANT: Charcy, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
COUNTRY:
USA

ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTIN ROLES

APPLICATION NUMBER: US/08/450,393A
PTLING DATE: MAY 25, 1995

TING DATE: MAY 25, 1995

THENDELING DATE: WAY 26, 1995
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5165
TELEPAK: 415-8857-0663
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STATE: California
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191 GlyProTyrPheProArgGlyTrpAsnAsn-PheHisThrIleMetArqAsnIleLeuGl
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APPLICANT: Grand J. et al.
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled NUMBER OF SEQUENCES: 56
CTGGTGTTCATCTTTGGTTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGC
                                                             114 AAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTT
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330 sGlnCysProValPheTyrArgGluThrValAspGlyValThrSerThrAsnThrProSe
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Patent No. 6132967
GENERAL INFORMATION:
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
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ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,669
FILING DATE: May 25, 1995
CLASSIFICATION: 435
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Mismatches:
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Matches:
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TELECOMONICATION INFORMATION:
TELEPRAN: 415-843-5000
TELEFRAN: 415-857-0663
TELEX: 380816CooleayPA
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Neeley, Richard REGISTRATION NUMBER: 30,092
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1331.00
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STATE: California
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APPLICANT: Graham, Gerard J. et al.
IIILE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
     110 yLeuValLeuProLeuLeuTleMetValIleCysTyrSerGlyIleLeuLysThrLeuLe
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OPERATING SYSTEM: PC-DOS/ANS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: US/09/534,185
FILLING DATE: 24 MAr-2000
CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/045,583 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 50, Application US/09534185 Patent No. 6403767 GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: Massachusetts
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CORRESPONDENCE ADDRESS:
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US-09-534-185-50
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COMPUTER: IND PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                 NAME: Mandraguera, Amy E.
REGISTRATION NUMBER: 36,207
REGERENCOPOCKET NUMBER: MAI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 maino acids
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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1331.00
83.76%
73.50%
50.65%
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internal
                                                                                ZIP: 02109
COMPUTER READABLE FORM:
                                                  Massachusetts
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Query Match:
                                                                      USA
                                   Boston
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FRAGMENT TYPE:
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                                                  STATE: M. COUNTRY:
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                                                                                 993 ATTCTTTGGCCTGAATAATTGCAGTAGCTCTAACAGGTTGGACCAAGCTATGCAGGTGAC 1052
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                                   290 rGluThrLeuGlyMetThrHisCysCysIleAsnProllelleTyrAlaPheValGlyGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: The Regents of the University of California TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT TITLE OF INVENTION: PROTEIN RECEPTORS
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US95/00476
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Conservative:
Mismatches:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                              350 rThrGlyGluGluGluValSerAlaGlyLeu 360
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NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-977-1001
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INFORMATION FOR SEQ ID NO: 4:
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ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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amino acid
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Best Local Similarity:
Query Match:
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Matches:
Conservative:
Mismatches:
Indels:
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NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                              MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                              LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                          TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
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1331.00
83.76%
73.50%
50.65%
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Best Local Similarity:
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DB:
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US-09-938-703-3 (1-1442) x PCT-US95-00476-4 (1-360)

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1113 GAAGTICAGAAACTACCICTINGICTICCIAAAAGCACATIGCCAAACGCTICIGCAA 1172
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                                                 CCCIGCCAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCA 353
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                                                                                                                   234 AACAAGATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAG
                                                               CIGGIGITCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGC
                                                                                                                                                       AAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTT
                                                                                                                                                                                                          474 ITCCTTCTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCCAGTGGGACTTTGGAAAT
                                                                                                                                                                                                                                                             534 ACAATGTGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTGGAATCTTCTTC
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Search completed: June 3, 2003, 18:52:47 Job time: 43.6947 secs us-09-938-703-3.rapb

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sequence 5, Appli
Sequence 2, Appli
Sequence 2, Appli
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Sequence 22, Appli
Sequence 22, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 6, Appli
Sequence 9, Appli
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Sequence 1,
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; Publication No. US20030092632A1
; GENERAL INFORMATION:
; APPLICANT: Dradic, Tatjana
; APPLICANT: Dradic, Wiliam C.
; TITLE OF INVENTION: SULFARED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 61010-Ab-1
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARR: Patentin version 3.1
; SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              352
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Matches:
Conservative:
Mismatches:
1 US-09-796-202-1
1 US-09-938-719-5
1 US-09-938-719-5
2 US-09-938-719-5
2 US-10-106-623-2
1 US-09-938-703-5
2 US-10-106-623-2
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1 US-09-938-719-9
1 US-09-938-719-4
1 US-09-938-719-4
1 US-09-938-719-4
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1745.50
96.60%
96.32%
66.42%
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   Percent Similarity:
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US-10-086-814-1
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    -MODEL-frame-intp. model -DEV-xlp
-Q-cgn2_1/USPTO_spool/US09938703/runat_03062003_161410_23015/app_query.fasta_1.1870
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-LCOPEL-0 -LCOPEXT-0 -UNITS-bits -STRT-1 -END-1 -MERIATA-biosun62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MXX-100
-THR_MIN-0 -ALIGN-15 -MODE-LCCAL -OUTFWT-ptc -NORM-ext -HEASIZE-560 -MINLEN-0
-TAR_MIN-0 -ALIGN-15 -MODE-LCCAL -OUTFWT-ptc -NORM-ext -HEASIZE-560 -MINLEN-0
-MAXLEN-200000000 -USER-USOBJ8703_GCGN 1.1_24_gunat_03062003_161410_23015
-NCPU-6 -ICPU-3 -NO_MMAP -LARGEGUERY -NEG_SCORES-0 -WAIT -DSPBLCCK-100
-LONGLOG -DEV_TIMBOUT-120 -WARN_IMBOUT-30 -THREADS-1 -XGAPOP=10 -XGAPEXT-0.5
-FGAPOP=6 -FGAPEXT-7 -YGAPOP=10 -YGAPEXT-0.5 -DELCAP-6 -DELEXT-7
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Sequence 14, Appl
Sequence 2, Appli
Sequence 15, Appl
                                                                                                                      (without alignments)
4506.655 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                               1 GAATTCCCCCAACAGAGCCA.....AGTAGATTAGATTC 1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                       June 3, 2003, 18:49:55; Search time 64.7773 Seconds
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13: /cgn2_6/ptodata/1/pubpaa/USOP_PUBCOMB.pep;*
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/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                             protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-086-814-1
US-09-734-221A-14
US-09-759-841-2
US-09-813-653-15
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                                                                                                                                                                                                                                                                                                                   383519 seqs, 101223694 residues
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Maximum Match 100%
Listing first 45 summaries
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0.5
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seq length: 200000000
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Match Length
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Perfect score:
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No.
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TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 CAAAAAATCAATGIGAAGCAAAATCGCAGCCGGCTCCTGCCTCCGCTTACTCACTGGTG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 GlnLysIleAsnValLysGlnIleAlaAlaArgLeuLeuProProLeuTyrSerLeuVal 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 AIGGATTATCAAGIGTCAAGICCAATCTAIGACATCAATTATTATACATCGGAGCCCTGC
                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/734,221A
FILING DATE: 11-Dec-2000
CLASSIFICATION: <URNown>
PRIOR APPLICATION: <URNown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/666,020
FILING DATE: 19-UN-1996
APPLICATION NUMBER: US 08/227,319
FILING DATE: 13-APR-1994
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-938-703-3 (1-1442) x US-09-734-221A-14 (1-352)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jackson Esq., David A. RECESTRATION NUMBER: 26,742
REFERBNE/POCKET NUMBER: 1049-1-004 I TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                            LANDAU, NATHANIEL R.
LIU, RONG
                            US/09734221A
                                                                                DENG, HONGKUI
ELLMEIER, WILFRIED
                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 352 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                          Sequence 14, Application US/09734; Publication 0. US20030096221A1 GENERAL INFORMATION: APPLICANT: LITTMAN, DAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.73e-158
1745.50
96.60%
96.32%
66.42%
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                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                             STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                               CITY: Hackensack
                                                                                                                                                                                                                                        Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                         IP: 07601
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RESULT 2
US-09-734-221A-14
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DB:
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           240 AIGGAITAICAAGIGICAAGICCAAICTAIGACAICAATIAITAIAACAICGGAGCCCIGC 299
                                                                  359
                                                                                                                     TICATCITIGGITITGTGGGCAACAIGCIGGICAICCICAICCIGAIAAACIGCAAAAGG 419
                                                                                                                                                                          CTGAAGAGCATGACTGACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT 479
                                                                                                                                                                                                                                  539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           806
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                          21 GlnLysileAsnValLysGlnIleAlaAlaArgLeuTeuProProLeuTyrSerLeuVal 40
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Matches:
Conservative:
Mismatches:
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FILE OF INVENTION: Assay Method
FILE REFERENCE: PC1034APME
CURRENT APPLICATION NUMBER: US/09/759,841
CURRENT FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: GB 0000663.5
PRIOR FILING DATE: 2000-01-12
PRIOR PRICK DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VET. 2.1
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1745.50
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US-09-759-841-2
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Best Local Similarity:
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                                                                                                                                      SEQ ID NO 2
LENGIH: 352
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APPLICANT: Dobbs, Susan
APPLICANT: Perros, Manoussos
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	Qy 420 CIGAAGAGCAIGACAFCTACCIGCICAACCTGGCCATCTCIGATTITCCIT 479	QY 480 CTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCCAGTGGGACTTTGGAAATACAATG 539	QY 540 IGTCAACTCTTGACAGGCTCTATTTATAAGGCTTCTTCTCGGAATCTTCTTCATCATC 599 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY 600 CICCIGACAATGGATAGGIACCIGGCIGTCGTCCATGCTGTGTTTGCTTTAAAAGCCAGG 659	QY 660 ACGCTCACCTTTGGGTGGTGACAAGTGTGACATCACTTGGGTGGTGGTTGCGTCT 719	OY 720 CTCCCAGGAATCATCTTTACCAGATCTCAAAAAGGAGGCTTCATTACACTGCAGCTCT 779	Qy 780 CATITICCATAC	OY 807 CITGGGGCTGGTGCTGCTTGTCATGGTCATCTGCTACTCGGGAATCCTAAAAAC 866	OY 867 TCTGCTTCGGTGTCGAAATGAGAAGAGCCACAGGGCTGTGAGGTTATCTTCACCAT 926	QY 927 CARGATEGITAATITCICITCIGGCCCCCTACAACAITGICCTICCCGGACCCCIT 986	QY 987 CCAGGAATTCTTTGGCCTGAATAATTGCAGTAGCTCTAACAGGTTGGACCAAGCTATGCA 1046	QY 1047 GGTGACAGAGACTCTTGGGATGACGCACTGCTTCATCATCTATGCCTTTGT 1106	Qy 1107 CGGGGAGAAGTICAGAAACTACCTCTTAGTCTTCTTCCAAAGCACATTGCCAAAGGCTT 1166	OY 1167 CTGCAAATGCTGTTCTATTTTCCAGCAAGGGCTCCCGAGCGAG	Oy 1227 CCGATCCACTGGGGACAGGAAATATCTGTGGGGCTTG 1263 	EI (A	; GENERAL INFORMATION: ; APPLICANT: Dragic, Tatjana ; APPLICANT: Olson, William ; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION ; FILE REFERENCE: 2048/61010/JPW/SHS ; CURRENT APPLICATION NUMBER: US/09/796,202
Db 220 rLeuLeuArgCysArgAsnGluLysLysArgHisArgAlaYalArgLeuIlePheThrII 240	QY 927 CATGATTGTTTATTTTCTCTTCTGGGCTCCCTACAACATTGTCCTTCTCCTGAACACTT 986	QY 987 CCAGGAATTCTTGCCTGAATAAVTGCTGCAGTAGCTCTAACAGGTTGGACCAAGCTATGCA 1046	OY 1047 GGTGACAGAGACTCTTGGGATGACGCTGCTGCATCAACCCCATCATCTATGCCTTTGT 1106	Qy 1107 CGGGGAGAAOTICAGAAACTACCICTIAGICTICTICCAAAAGCACTGCCAAACGCTT 1166 Db 300 lGlyGluLysPhcArgAsnTyrLeuLeuValPhePhcGlnLysHisIleAlaLysArgPh 320	Qy 1167 CTGCAAATGCTGTTCTATTTCCAGCAAGGCTCCCGAGCAAGCTCAGTTTACAC 1226	Qy 1227 CCGATCCACTGGGGAGCAGGAATATCTGTGGCTTG 1263 	RESULT 4 US-09-813-653-15 ; Sequence 15, Application US/09813653 : Patent No. US/00020064770A1	. 0	APPLICANT: Tan Hehir. Christina TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds FILE REPRESERBINE: NS-08-08 FILE REPRESERBINE: CMS-08-08			01) ORGANISM: Homo sapiens US-09-813-653-15 Alignment scores.	Pred. No.: 1.73e-158 Length: 352 Score: 1745.50 Matches: 340 Percent Similarity: 96.00% Conservative: 1 Best Lonal Similarity: 96.32% Mismatches: 0	66.42% Indebs: 10 Gaps: 42) x US-09-813-653-15 (1-352)	Qy 240 ATGGATTATCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC 299	Qy 300 CAAAAAATCAATGTGAAGCAAATCGCAGCCCCCTCCTGCCTCTACTCACTGGTG 359

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1107 CGGGGAGAAGTICAGAAACTACCTCTTAGTCTTCCAAAAGCACATGCCAAACGCTT 1166
                                                                                                                                            TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                  300
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                                        280 nValIhrGluIhrLeuGlyMetIhrHisCysCysIleAsnProIleIleIyrAlaPheVa
                                                                                         eGlnGluPhePheGlyLeuAsnAsnCysSerSerAsrAsnArgLeuAspGlnAlaMetGl
                         GGTGACAGAGACTCTTGGGATGACGCACTGCTGCATCAACCCCATCATCTATGCCTTTGT
                                                                                                                                COMPART. CA.

CONTRET READABLE FORM:

AMDIUM TYPE: Floppy disk
COMPUTER: ELEMP PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,719
FILING DATE: 24-Aug-2001
CLASSIFTARION: CURROWN:
PRIOR APPLICATION NAMER: 09/626,939
FILING DATE: 27-JULY-2000
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 34,115
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                          Sequence 5, Application US/09938719 Patent No. US20020106742A1 GENERAL INFORMATION:
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Matches:
Conservative:
Mismatches:
Indels:
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1745.50
96.60%
96.32%
66.42%
         NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
CURRENT FILING DATE:
                                                              TYPE: PRT
ORGANISM: human
                                                                                                                  Alignment Scores:
                                                  LENGIH: 352
                                                                                       US-09-796-202-1
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US-09-939-226-5

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APPLICANT: SARBOUNTER, MARC
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
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ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/939,226

FILING DATE: 24-Aug-2001

CLASSIETCATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
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REGISTRATION NUMBER: 34,115
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Sequence 5, Application US/09939226
Patent No. US20020110805A1
GENERAL INFORMATION:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ :
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1745.50
96.60%
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                                                            APPLICANT: SAMSON, MICHEL
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Best Local Similarity:
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                  (EPO)
   SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                REFERENCE/DOCKET NUMBER: <Unknown>
                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
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                                                                    CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                  NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ
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1745.50
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                                                                                                                                                                                                                                                                                                                                                             CTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTTCATTACACTGCAGCTCT
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                                             CTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATGCTGTGTTTGCTTTAAAAGCCAGG
                                                                                                       STREET: 520 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGATCCACTGGGGAGCAGGAAATATCTGTGGGGCTTG 1263
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ADDRESSEE: Knobbe, Martens, Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Patent No. US2020110870A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBERT, FREDERICK
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VASSART, GILBERT
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                NAME/KEY: misc_feature
OTHER INFORMATION: /- "88C amino acid sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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340
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
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Pred. No.:
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                                                          CATGATTGTTTATTTTCTCTGGGCTCCCTACAACATTGTCCTTCTCCTGAACACCTT
                                                                                                                                                                           GGTGACAGAGACTCTTGGGATGACGCACTGCTGCATCAACCCCATCATGTTGT
                                          TCTGCTTCGGTGTCGAAATGAGAAGAAGAGGCACAGGGCTGTGAGGCTTATCTTCACCAT
Schweickart, Vicky L.
Raport, Carol J.
TITLE OF INVENTION: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: 111inois COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODMETING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                            1227 CCGATCCACTGGGGAGCAGGAATATCTGTGGGCTTG 1263
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/106,623
FILING DATE: 26-Mar-2002
CLIASSIFICATION: -(Unknown)-
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/771,276
PRIOR DATE: -(Unknown)-
APPRING DATE: -(Unknown)-
APPRING PARE: CANANON-
APPRING AGENT INFORMATION:
NAME: No. US/20020150888Aland, Greta E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 352 amino acids TYPE: amino acid
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Patent No. US20020150888Å1
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Db 101 CysGlnLeuLeuThrGlyLeuTyrPheIleGlyPhePheSerGlyIlePheIleIle 120	Qy 600 CTCCTGACAATGGTACCTGGCTGTCCTGCTGTGTTTGCTTTAAAAGCCAGG 659	QY 660 ACGGTCACCTITGGGTGACAAGTGTGATCACTIGGTGGCTGGTGTTTGCGTC 7.19	QY 720 CTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTTCATTACACCTGCAGCTCT 779	QY 780 CATTTCCATAC	QY 807 CTTGGGGCTGGTCCTGCCTGCTTGTCATGGTCATCTGGGGAATCCTAAAAAC 866	Qy 867 TCTGCTTCGGTGTCGAAATGAGAAGAGGCACAGGGCTGTGAGGCTTATCTTCACCAT 926	Qy 927 CATGATTGTTTATTTTCTCTGGGCTCCCTACAACATTGTCCTTCTCGGACACCTT 986	Qy 987 CCAGGAATTCTTTGGCCTGAATAGCAGTAGCTCTAACAGGTTGGACCAAGCTATGCA 1046	OY 1047 GGTGACAGAGACTCTTGGGATGACGCTGCAGCGATCAACCCCATCTATGCCTTTGT 1106	OY 1107 CGGGGGAGAAGTTCAGAAACTACCTCTTAGTCTTCTCCAAAAGCACATTGCCAAACGCTT 1166	OY 1167 CTGCAAANGCTGTTCTATTTTCCAGCAAGAGGCTCCCGAGGAAGAAGCTCAGTTTACAC 1226	OY 1227 CCGATCCACTGGGGACCAGGAAATATCTGTGGGCTTG 1263	RESULT 11 US-10-232-686-2 ; Sequence 2, Application US/10232686 ; Publication No. US20030023044A1	; GENERAL INFORMATION: ; APPLICANT: Li, Y. Steven M. ; APPLICANT: Ruben, Steven M. ; TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10	; FILE REFERENCE: 1468.11500N ; CURRENT APPLICATION NUMBER: US/10/232,686 ; CURRENT FILING DATE: 2022-09-03 ; PRIOR APPLICATION NUMBER: 09/339,912	; PRIOR FILING DATE: 1999-06-25; PRIOR APPLICATION NUMBER: 09/195,662; PRIOR FILING DATE: 1998-11-18; PRIOR PILING DATE: 08/466,343	; PRROP FILING DATE: 1995-06-06 ; NUMBER OF SEQ ID NOS: 9 ; SOFTWARE: PatentIn version 3.0 ; SEQ ID NO 2 ; LENGTH: 352 ; TRYPE: DRY
	OY 1107 CGGGGAGAAGTTCAGAAACTACCTCTTAGTCTTCCAAAAGCACATTGCCAAACGCTT 1166	Qy 1167 CTGCAAATGCTGTTCTATTTTCCAGCAGAGGCTCCCGAGCGAG	Qy 1227 CCGATCCACTGGGGAGCAGGAATATCTGTGGCCTTG 1263	RESULT 10 US-09-813-653-17 Sequence 17, Application US/09813653 Datest No. TESOGOROGATION	; GENERAL INFORMATION: ; APPLICANT: Nestor, John ; APPLICANT: Wilson, Carol ; APPLICANT: See		CURRENT FILING DATE: 2001-03-20 PRIOR APPLICATION NUMBER: US 60/190,946 PRIOR FILING DATE: 2000-03-21 PRIOR FILING DATE: 2000-03-21		NOTES OF THE NOTE OF THE NOTE OF THE NOTES O	CRGANISM: Homo sapiens US-09-813-653-17		66.19% Indels: 10 Gaps: 2) x US-09-813-653-17 (1-352)	Qy 240 ATGGATTATCAAGTGCAAGTCCAATCAATAATATTATACAGGCCCGC 299	OY 300 CAAAAAATCAAJGAAGCAAAATCGCAGCCCGCCTCCGCTCTGCTCACTCAGGG 359	OY 360 TTCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGG 419	Qy 420 CTGAAGAGCATGACTCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT 479	QY 480 CTTACTGTCCCCTTCTGGGCTCACTATGCTGCGCCCAGTGGGACTTTGGAAATACAATG 539

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CGGGGAGAAGTICAGAAACTACCTCTTAGTCTTCTTCCAAAAGCACATTGCCAAACGCTT 1166
                                                        240 AIGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC 299
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              21 GlnLysIleAsnValLysGlnIleAlaAlaArgLeuLeuProProLeuTyrSerLeuVal
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                 ; Sequence 2, Application US/09725285
; Patent No. US20010000241A1
; GENERAL INFORMATION:
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1737.50
96.32%
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Best Local Similarity:
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DB:
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                                                                                                                                        US-09-725-285-2
  1107
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; ORGANISM: Homo saplens
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                                                          Percent Similarity:
Best Local Similarity:
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                               Alignment Scores:
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/ ORGANISM: Homo sapiens US-09-779-879A-22 Alignment Scores: 1.01e-157 Length: 352 Score: 1737.50 Matches: 339 Percent Similarity: 96.32% Conservative: 1 Best Local Similarity: 96.03% Mismatches: 1 Query Match: 66.11% Indels: 12 DB: US-09-938-703-3 (1-1442) x US-09-779-879A-22 (1-352)	Qy 240 ATGGATATCAAGIGTCAAGTCCAATCTATGACATCAATTATTATACATGGAGCCCTGC 299	Qy 300 CAAAAAAICAAGGAAAACGAAATGGCGGCCCCCCCGGCTCCGCTCTACTCACTGGTG 359	Qy 360 TICATCITIGGITITIGIGGCAACAIGCTGGTCAICCICAICCIGAIAACIGCAAAGG 419	Qy 420 CTGAAGAGCATGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT 479	Qy 480 CITACIGICCCTICTGGGCTCACIAIGCIGCCGCCCAGTGGGACTTIGGAAAIACAAIG 539	Qy 540 IGTCAACICTTGACAGGGCTCTATITTATAGGCTTCTTCTCTGGAAICTTCTTCATC 599	OY 600 CICCIGACAAIGGIAGGIACCIGGCIGICGICCAIGCIGITGCIITAAAAGCCAGG 659 	Qy 660 ACGGTCACCTTTGGGGTGACACAGTGTGATCACTTGGGTGGTGGTGTTTGCGTCT 719	OY 720 CTCCCAGGAATCATCTTACCAGATCTCAAAAAGAGGTCTTCATTACACCTGCAGCTCT 779	Qy 780 CATTTCCATAC
Qy GOO CTCCTGACAATCGATAGGTACCTGGCTGTCGTCGTGTTTGCTTTAAAAGCCAGG 659	Qy 780 CATTTCCATAC	QY 807 CITGGGGCTGCTGCCGCTGCTGTCATGGTCATCTGCTACTCGGGAATCCTAAAAAC 866	QY 867 TCTGCTTCGGTCGAAATGAGAAGAGGCACAGGCTGTGAGGCTTTGACCAT 926 	QY 927 CATGATTGTTTTTCTCTTGGGCTCCCTACATTGTCCTTCTCCTGAACACTT 986	Qy 987 CCAGGAATTCTTGGCCTGAATAATTGCAGTAGCTCTAACAGGTTGGACCAAGCTATGCA 1046	QY 1047 GGTGACAGAGACTCTTGGGATGACGCACTGCATCAACCCCATCATCTATGCCTTTGT 1106	Qy 1107 CGGGGAGAAGTTCAGAAACTACCTCTTAGTCTTCTCCAAAAGCACATGCCAAAGCGCTT 1166 	QY 1167 CIGCAAAIGCIGITCIAITITCCAGCAAGAGCICCCGAGCGAGCAAGCICAGITIACAC 1226 	Qy 1227 CCGATCCACTGGGGGAGCAGGAATATCTGTGGGGCTTG 1263 Db 340 rArgSerThrGluGluGluIleSerValGlyLeu 352	RESULT 13 15-09-779-8794-22 15-Sequence 22, Application US/09779879A 15-Sequence 22, Application US/09779879A 15-Sequence 22, Application US/09779879A 15-Sequence 22, Application US/09779879A 15-Sequence 22, Application US/097798A 15-Sequence 25, Application US/097798A 15-Sequence 25, Application Charles 2000A 15-Sequence 26, Application Charles 2000A 15-Sequence 26, Application UNIMBER: US/09/779,879A 15-Sequence 26, Application UNIMBER: US/09/779,879A 15-Sequence 2000A 15-Sequence 26, Application UNIMBER: US/09/181,258 15-Sequence 2000A 15-Sequence 2000A 15-Sequence 2000A 15-Sequence 2000A 15-Sequence 2000A 15-Sequence 200A 15-Seq

QY 600 CTCCTGACAATGGAAGGTACCTGGCTGTCGTCGTGTTTGCTTTAAAAGCCAGG 659 121 LeuleuThrIleAspargTyrLeualaValValHisAlaValPheAlaLeuLysAlaArg 140 Qy 660 AGGTCACCTTTGGGGTGACAAGTGTGATCATTGGGTGGTGGTTTGCTTTGCGTCT 719 141 ThrValThrPheGlyValValThrFill	
0y 1107 CGGGGAAGTTCAGAAACTACCTCTTAGTCTTCCAAAAGCACATTGCCAAACGCTT 1166 1107 CGGGGAAGTTCAGAAACTACCTCTTCTTCCAAAAGCACATTGCCAAACGCTT 1166 1207 LGLJYSPheATGASTTYLEULEUVALPhePheGlnLySHisILeAlaLySArgPh 320 0y 1167 CTGCAAAATGCTGTTTTTCCAGCAAGAGGCTCCCGAGCGAG	### RESULD 14 ### SECURE 14 ### SE

us-09-938-703-3.rapb

1737.50 Matches: 7: 96.32% Conservati rity: 96.03% Mismatches 66.11% Indels: 10 Gaps:	-703-3 (1-1442) x US-09-195-6628-2 (1-352) 240 хмссхишилисх хустопоз хотосский технологист хителист сост	<pre>4.0 ALGGARIALCHAGAICLAALCIATGARITATATATATATATAGAGCCCTGC 299 1 </pre>		otherstransurarnjaciniteriaariahearitorioriorioriorioriorioriorioriorioriorio	0 4	420 CTGAAGAGCATGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT 479	480 CTTACTGTCCCCTTCTGGGCTCACTAIGCTGCCGCCCAGTGGGCTTTGGAAATACAATG 539	59 5	CCCTGGAATCGATCGATACCTGCTGCTCCTCTGTTTTGTTTAAAAGCCAGG 65	121 LeuLeuThrileAspArgTyrLeuAlaValValHisAlaValPheAlaLeuLysAlaArg 140	660 ACGGLCACCTTTGGGGTGGTGAAAGTGTGATCACTTGGGTGGTGGTGGTGTTTGCGTCT 719 	720 CTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTTCATTACACCTGCAGCTCT 779	80 CATTTCCATACATTAAAGATAGTCAT 80		807 CTIGGGGCTGGTCCTGCTCGTTGTCATGGTCATCTGCTACTCGGGAATCCTAAAAAC 866 	867 TCTGCTTCGGTCCGAAATGAGAAGAAGAGCCTACGGCCTGTGAGCCTTATCTTCACCAT 926 	98	140 eMetileValryrPheLeuPheTrpAlaProTyrAsnIleValLeuLeuLeuSnThrPh 260	987 CCAGGAAITCTITGCCTGAATAAVIGCAGIAGCTCTAACAGGITGGACCAAGCIAIGCA 1046 	1047 GGTGACAGAGACTCTTGGGATGACGCACTGCATCAACCCCATCATCTATGCCTTTGT 1106 	07 CGGGGGGAGAGGTCAGAAACTACCTCTTAGTCTTCCAAAAGCACATTGCCAAACGCTT	
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Qy	1227 CCGATCCACTGGGAGCAGGAAATATCTGTGGGCTTG 1263
qq	340 rArgserthrGluGluGluGluIleserValGlyLeu 352

Search completed: June 3, 2003, 19:13:30 Job time: 83.7773 secs

G protein-coupled G protein-coupled G protein-coupled G protein-coupled interleukin-8 rece interleukin-8 rece

JC5068 165989

638.5 573.5 559.5 552.5 528.5 511.5 507 505 501.5

A45680

A55735

interleukin-8 rece interferon-inducib

A53611 A48921 JQ1231 JE0349 A53752 JN0621

A39445 G00048 A45747 S42096 S28787

G protein-coupled interleukin-8 rece interleukin-8 rece

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RESULT 1
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-VOCREL-frame. 1.02p.model - DEV-x1p
-Q-Cgg12_1/USFPV-108109939103/yrunat_03062003_161407_22855/app_query.fasta_1.1870
-DB-PIR_73 - OFPWT-fastan - SUFFIX-rpr - MINMAPCH-0.1 - LOOPEL-0 - LOOPEXT-0
-UNITS-Dits -START-1 - END--1 - MATRIX-blosum62 - TRANS-human40.cdi - LIST-45
-UNITS-Dits - START-1 - END--1 - MATRIX-blosum62 - TRANS-human40.cdi - LIST-45
-UNITS-Dits - START-1 - FRD--1 - MATRIX-blosum62 - TRANS-15- - MODE-LOCAL
-UNITS-Dits - START-1 - FRD--1 - MATRIX-BLOSUM000000
- USER-US09938703_6CGN_1 1 - 89_6runat_0306203_161407_22855 - NCPU-6 - ICPU-3
-NO_MMAP - LARGEQUERY - MASC_SCORES-0 - WAIT - DSPBLCCX-100 - LONGLOG
-DBV_TIMEOUT=120 - WARN_TIMEOUT=30 - THREADS-1 - XGAPOP=10 - XGAPORT-0.5 - FGAPOP=6
-FGAPEXT-7 - TGAPOP-10 - YGAPDXT-0.5 - DELEXT-7
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                                                                                                                                                                                                                                                                                                                                                                                          GAATTCCCCCAACAGAGCCA.....AGTAGATTAGATCCGAATTC 1442
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                     protein search, using frame_plus_n2p model
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XGAPOP 10.0, XGAPEXT
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fusin (LESTRA) - c neuropeptide Y/pep interleukin-8 rece neuropeptide Y/pep G protein-coupled anglotensin II rec anglotensin II rec

A42656 JC2134 S44425 S15403

S42628

492.5 491.5 491.5 486 483.5

G protein-coupled angiotensin II rec angiotensin II rec angiotensin II rec

ALIGNMENTS

G protein-coupled angiotensin II rec

\$26667 JQ1516

S56162

JH0621

A43113	
chemokine (C-C) receptor 5 - human	
N;Alternate names: C-C CKR-5; CCR5	
C; Species: Homo sapiens (man)	
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000	on 12-Jul-1996 #text_change 20-Jun-2000
C; Accession: A43113; S71808; A58834; A58832; G02653; A5	A58832; G02653; A58833
R; Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.	J.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996	
A; Title: Molecular cloning and functional expression of	ional expression of a new human CC-chemokine rece
A; Reference number: A43113; MUID:96241590; PMID:8639485	11590; PMID:8639485
A; Accession: A43113	
A; Molecule type: mRNA	
A; Residues: 1-352 <sam1></sam1>	
A; Cross-references: GB: X91492; NID: q1262810; PIDN: CAA62796.1; PID: q1262811	1262810; PIDN:CAA62796.1; PID:q1262811
R; Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Sarac	J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Sarac
M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman,	th, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.
Nature 382, 722-725, 1996	
A; Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant allele	on in caucasian individuals bearing mutant allele
A; Reference number: S71808; MUID:96345670; PMID:8751444	45670; PMID:8751444
A; Accession: S71808	
A; Status: nucleic acid sequence not shown; not compared with conceptual translation	shown; not compared with conceptual translation
A; Molecule type: DNA	•
A; Residues: 182-206;207-230 <sam2></sam2>	
A; Accession: A58834	
A; Status: nucleic acid sequence not shown; not compared with conceptual translation	shown; not compared with conceptual translation
A; Molecule type: DNA	
A; Residues: 1-184, 'IKDSHLGAGPAAACHGHLLLGNPKNSASVSK' <sa< td=""><td>JLLGNPKNSASVSK' <sam3></sam3></td></sa<>	JLLGNPKNSASVSK' <sam3></sam3>
A; Cross-references: GB: X99393; NID: 91524062; PIDN: CAA67767.1; PID: 91524063	1524062; PIDN:CAA67767.1; PID:g1524063
A; Note: this frameshift mutation results in a non-functional receptor but confers	ults in a non-functional receptor but confers a
nd may have had a selective advantage by conferring res	by conferring resistance to Yersinia plague ini
R; Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.	ıy, H.L.; Murphy, P.M.
J. Leukoc. Biol. 60, 147-152, 1996	
A)Title: Cloning and functional expression of CC CRR5, a human monocyte CC chemokine	ession of CC CKR5, a human monocyte CC chemokine
A; Relefence number: Abbs32; MULD:952959/0; PMLD:8599119 A:Accession: A58832	PATD: BRID: BB 99119
A; Molecule type: mRNA	
A; Residues: 1-352 <com1></com1>	

chemokine (C-C) re chemokine (C-C) re chemokine (C-C) re chemokine (C-C) re

chemokine (

JC2443 I38450 A45177

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149341 149339 G02436 A57160 JC4587 S55594

3352 3360 33760 3355 33560 33560 33560 33560 3356

953

891.5 878.5 797.5 776 716 688.5

Description

A

В

Length

Query

Score

Result No.

SUMMARIES

MIP-1 alpha recept macrophage inflamm

chemokine (C-C) re chemokine (C-C) re chemokine (C-C) re g protein-coupled MIP-1 alpha recept G protein-coupled

probable G protein orphan G protein-c

JC5067 I58186 JC4304 I49340

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Cyccession: JC2443; I18463

R; Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A; Title: CDNA cioning and functional expression of a human monocyte chemoattractant p
A; Reference number: JC2443; MUID:94324942; PMID:8048929
A; Molecule type: mRNA
A; Residues: 1-360 CYAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chemokine (C-C) receptor 2, splice form B - human
N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte c
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1995 *sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: DDBJ:D29984; NID:9531246; PIDN:BAA06253.1; PID:9531247
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant A;Reference number: A53477; MUID:94195821; PMID:8146186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGGAATICITIGGCCTGAATAATIGCAGIAGCTCTAACAGGITGGACCAAGCTATGCA 1046
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                                                                                                                                                        ThrValThrPheGlyValValThrSerValIleThrTrpValValAlaValPheAlaSer 160
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                                                                      CTCCCAGGAATCATCTTACCAGATCTCAAAAAGAAGGTCTTCATTACACCTGCAGCTCT
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                                               CTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATGCTGTTTGCTTTAAAAGCCAGG
                                                                                                                                                                                                                                                                                             ------ATTABAGATAGTCAT
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A; Residues: 1-89, L', 91-352 <COM2>
A; Residues: 1-89, L', 59-352 <COM2>
B; Raport, C.J.; Goaling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
J. Miol. Chem. 271, 17161-17166, 1996
A; Title: Molecular cloning and functional characterization of a novel human CC chemokine
A; Reference number: A58833; MUID:96291862; PMID:8663314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A. Description: G protein-coupled receptor for chemokines MIP-lalpha, MIP-lbeta and RANTH A: Note: probably acts to control granulocyte proliferation and differentiation C. Superfamily: vertebrate rhodopsin C. Superfamily: vertebrate rhodopsin C. Superfamily: protein-coupled receptor; glycoprotein; phosphoprotein; transmembran F: 32-56/Domain: transmembrane *status predicted <TML>
F: 67-87/Domain: transmembrane *status predicted <TML>
                                                                                                                                                                                                                                                                                                                                     Cross-references: GB:U54994; NID:g1457945; PIDN:AAC50598.1; PID:g1457946
Comment: This is a receptor for chemokines MIP-lalpha (see PIR:A30574), MIP-lbeta (see
Comment: Macrophage and dual-tropic strains of HIV-1 bind to a complex of chemokine (
A; cross-references: GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:g1502409
A; Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R; Combadiere, C.
submitted to the EMBL Data Library, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 AIGGATTAICAAGIGICAAGICCAAICIAIGACAICAATIATIAIAACAICGGAGCCCIGC 299
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F;268/Binding site: carbohydrate (Asn) (covalent) *status predicted
F;336,337,342/Binding site: phosphate (Ser) (covalent) *status predicted
F;340,343/Binding site: phosphate (Thr) (covalent) *status predicted
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340
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12
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A;Cross-references: GDB:1230510; OMIM:601373
A;Map position: 3p21-3p21
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Matches:
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                                                                             A;Reference number: H01541
A;Accession: G02653
A;Status: translated from GB/EMBL/DDBJ
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1745.50
96.60%
96.32%
66.42%
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A, Molecule type: mRNA
A, Residues: 1-352 (RAPA
A, Cross-references: GB:U5
C, Comment: This is a rece
C; Comment: Macrophage an
C; Genetics:
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Hest Local Similarity:
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us-09-938-703-3.rpr

uArgCysArgAsnGluLysLysArgHisArgAlaValArgValIlePheThrIleMetII 250 IGTTTATTTTCCTTCTGGGCTCCCTACAACATTGTCCTTCTCGAACACCTTCCAGGA 992	ulysPheArgArgTyrieuSerValPhePheArgTysHisIleThrLysArgPheCysty 330 ATGCTGTTCTATTTCCAGCAAGAGGCTCCCGAGCGAGCAGCTCAGTTACACCCGATC 1232	INBA50 Chemokine (C-C) receptor 2, splice form A - human Chamokine (C-C) receptor 2, splice form A - human Chamokine (C-C) receptor 2, splice form A - human C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999 C; Accession: 138450 R; Charo, I.F.: Wwers, S.I.: Herman, A : Franci, C : Connolly A I : Couchity G B	ง ซี. ม	19D:337364; OMIM:601267 3p21 rate rhodopsin live splicing; G protein-coupled receptor; glycoprotein; transmemb membrane #status predicted <tml> smembrane #status predicted <tml></tml></tml>	Insmembrane #status predicted <tm3> Insmembrane #status predicted <tm4> Insmembrane #status predicted <tm4> Insmembrane #status predicted <tm6> Insmembrane #status predicted <tm6> Insmembrane #status predicted <tm6> Insmembrane #status predicted <tm7> Inspendicted (Asn) (covalent) #status predicted Iliide bonds: #status predicted</tm7></tm6></tm6></tm6></tm4></tm4></tm3>	6.07e-97 Length: 374 1191.00 Matches: 234 83.86% Conservative: 31 74.05% Mismatches: 34 45.32% Indels: 17 2 Gaps: 4	703-3 (1-1442) x 138450 (1-374) 234 AACAAGATGGAITATCAAGTGTCAAGTCCAATCTATGACATTATTATACATGGAG 293 11 ::: 14 AsnGluSerGlyGluGluValThrThrPhepheAspTyrAspTyrGlyAla 30 294 CCCTGCCAAAAAATGTGAAGGAAATGGAGGGGGGCCGCCTCGGCTCTACTCA 353
Al9120.1; PID:g472558 Db 230	360 258 300 310 258 258 258 36 36 36 36 370 11 273 3 370 3 173 3 370 3 370 3 370	TATACATCGGAG 293Glyala 30 CCGCTCTACTCA 353 ProLeulyriser 50	TAAACTCC 413 A.A.	533	TTTAAAA 653 aLeuLys 150 TGTGTT 713 	ACACCTGC 773 	DS-09-938-
A;Cross-references: EMBL:U03905; NID:g472557; PIDN:AAA19:C;Genetics: A;Gene: GDB:CMKBR2 A;Cross-references: GDB:337364; OMIM:601267 A;Map position: 3221-3721 C;Superfamily: vertebrate rhodopsin C;Keywords: alternative splicing; G protein-coupled recepts; 43-70/Domain: transmembrane #status predicted <tm2>F;81-10/Domain: transmembrane #status predicted <tm2>F;81-115-136/Domain: transmembrane #status predicted <tm3>F;154-178/Domain: transmembrane #status predicted <tm3>F;244-268/Domain: transmembrane #status predicted <tm4>F;247-266/Domain: transmembrane #status predicted <tm5>F;247-266/Domain: transmembrane #status predicted <tm5>F;147-1409/Jomain: transmembrane #status predicted <tm5>F;147-1409/Jomain: transmembrane #status predicted <tm5>F;147-1409/Jomain: transmembrane #status predicted <tm5>F;147-1409/Jomain: transmembrane #status predicted <tm5>F;147-140000000000000000000000000000000000</tm5></tm5></tm5></tm5></tm5></tm5></tm4></tm3></tm3></tm2></tm2>	Alignment Scores: Pred. No.: Score: Score: 1331.00 Matches: Percent Similarity: Bast Local Similarity: 73.50% Wismatches: Ouery Match: 50.65% Indels: DB: US-09-38-703-3 (1-1442) x JC2443 (1-360)		QY 354 CTGGTGTTCATCTTTGGTTTTGTGGCAACATGCTGGTCATCCTGATAACTGC	OY 474 ITCCTTCTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCCAGTGGGACTTTGGAAAT	Oy 594 ATCATCCTCCAGATCGATAGGTACCTGGCTGCTCCATCGTGTGTTTG	Qy 714 GCGTCTCTCCCAGGAATCATCTTTACCAGATCTCAAAAAGGAGGTCTTCATT	Qy 813 GCTGGTCCTGCCTGTCATGTCATCTGCTACTCGGGAATCCTAAAAACTCTGCT

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A; Gene: GDB:CMKBRI; CMKR-1
A; Gene: GDB:CMKBRI; CMKR-1
A; Gene: GDB:CDB:138446; OMIM:601159
A; Map position: 3p21-3p21
C; Superfamily: vertebrate rhodopsin
C; Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein;
C; Keywords: disulfide bond; G protein-coupled crmi>
F; 36-60/Domain: transmembrane #status predicted crmi>
F; 316-129/Domain: transmembrane #status predicted crmi>
F; 147-171/Domain: transmembrane #status predicted crmi>
F; 205-223/Domain: transmembrane #status predicted crmi>
F; 205-223/Domain: transmembrane #status predicted crmi>
F; 205-223/Domain: transmembrane #status predicted crmi>
F; 346-305/Domain: transmembrane #status predicted crmi>
F; 388-305/Domain: transmembrane #status predicted crmi>
F; 385/Binding site: carbohydrate (Ser) (covalent) (by casein kinase II) #status predicted F; 345/Binding site: phosphate (Ser) (covalent) (by casein kinase II)
                                                                                                   A:Itle: Structure and functional expression of the human macrophage inflammatory 1 A;Reference number: I55671; MUID:93240122; PMID:7683036
A;Accession: I55671
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LysValAsnGluArgAlaPheGlyAlaGlnLeuLeuProProLeuTyrSerLeuValPhe 45
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9 AspTyrAspThrThrThrThr-----GluPheAspTyrGlyAspAlaThrProCysGln
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LysAsnMetThrSerIleTyrLeuLeuAsnLeuAlaIleSerAspLeuLeuPheLeuPhe
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                 A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
                                                                                                                                                                                                   A; Cross-references: GB:L10918; NID:9292416; PIDN:AAA36543.1; PID:9292417
                                    A; Experimental source: HL60 cells
A; Note: sequence extracted from NCBI backbone (NCBIP:124876)
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Matches:
Conservative:
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A;Molecule type: mRNA
A;Residues: 1-355 <RES>
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                                                                                     Exp. Med. 177, 1421-1427, 1993
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N'Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Accession: A45177; I5561
R; Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
Cell 72, 415-425, 1993
A; Reference number: A45177; MUID:93161416; PMID:7679328
A; Reference number: A45177
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             993 ATTCTTIGGCCIGAATAATIGCAGIAGCICTAACAGGTIGGACCAAGCIAIGCAGGIGAC 1052
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                                               CTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGC
                                                                                                                                                                              TTCCTTCTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCCAGTGGGAACTTTGGAAAT
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macrophage inflammatory protein-1 alpha receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul1-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: 149339
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17444-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chem A;Reference number: 149339; MUID:95340546; PMID:754241
A;Accession: 149339
A;Status: preliminary; translated from GB/EMBL/DDBJ
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             399 AICCIGATAAACIGCAAAAGGCIGAAGAGCAIGACIGACATCIACCIGCICAACCIGGCC 458
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                             221 eCysTyrSerGlyIlelleLysThrLeuLeuArgCysProAsn---LysLysLysHisLy
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                                                                 159 ATCTCTGACCTGTTTTTCCTTCTTACTGTCCCCTTCTGGGCTCACTATGCTGCC---GCC
                                                                                                                     CAGTGGGACTTTGGAAATACAATGTGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTC
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nValThrGluValIleAlaTyrThrHisCysCysValAsnProValIleTyrAlaPheVa 304
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C;Date: 02-Jul-1996 *sequence_revision 02-Jul-1996 *text_change 02-Jul-1998
TCTGCTTCGGTGTCGAAATGAGAAGAAGAGGCACAGGGCTGTGAGGCTTATCTTCACCAT
                                                                                                                                                                                            CATGATTGTTTATTTTCTCTTCTGGGCTCCCTACAACATTGTCCTTCTCCTGAACACCTT
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Matches:
Conservative:
Mismatches:
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A:Molecule type: DNA
A:Residues: 1-359 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIP-1 alpha receptor like-2 - mouse
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A; Molecule	A: Molecule type: DNA A: Residues: 1-355 < RES	අ	293 sCysCysVa]
A; Cross-ret C; Superfami	A;Cross-references: EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548 C:Superfamily: vertebrate rhodopsin	ογ	1134 AGTCTTCTTC
Alignment Scores	COLDER.	qa	113 gGlnLeuPhe
Pred. No.: Score:	6.34e-76 Length: 953.00 Matches:	δδ	1194 AGAGGCTCCC
Percent Similarity Best Local Similar	: 69.978 Conservative: itv: 53.948 Mismatches:	đ	333 lAspGlnLe
Query Match DB:	: 36.26% Indels: 2 Gaps:	Qy	1254 TGTGGGC 13
US-09-938-7	US-09-938-703-3 (1-1442) x 149339 (1-355)	셤	352 raladiy 35
0y 2	270 GACATCAATTATTATATACATCGGAGCCCTGCCAAAAATCAATGTGAAGCAAATCGCAGCC 329	RESULT G02436	
Dp	15 GluPheAspTyrGlyAspSerThrProCysGlnLysThralaValArgAlaPheGlyAla 34	N;Alternat	cnemokine (c-c) receptol N;Alternate names: C-C (
දුරු අධ	330 CGCCTCCTGCCTCCCCTCTACTCACTGGTGTTTAGGTTTTGTGGGCAACATGCTG 389	C; Date C; Acce R: Pona	Crate: 21-Dec-1996 #sec Crate: 21-Dec-1996 #sec Cracession: G02436; AS: R:Ponath: P.D.
Oy 3	390 GTCATCCTCATCCTGATAAACTGCAAAAGGCTGAAGAAGACTGACT	submit A; Refe	submitted to the EMBL Day, Reference number: H012
Dp	55 ValileLeuValLeuMetGlnHisArgArgLeuGlnSerMetThrSerIleTyrLeuPhe 74	A; Acce A; Stat	ssion: GUZ436 us: translated fr
Qy 4	450 AACCIGGCCAICTCTGACCIGITITICCTICTITACTGCCCCCTICTGGGCTCACTAIGCT 509	A; MOLE A; Resi A: Cros	cuie cype: DNA dues: 1-355 <pon> s-references: FMB</pon>
	75 AsnieualavalSerAspieuvalPheleuPheThrieuProPheTrpileAspTyriys 94	R; Comb	adiere, C.; Ahuja 1. Chem. 270. 164
		A; Titl	e: Cloning and furence number: A57
අු	95 LeuLysAspAspTrpllePheGlyAspAlaMetCysLysLeuLeuSerGlypheTyrTyr 114	A; Acce	ssion: A57237
ko ta	567 ATAGGCTTCTTCTCTGGAATCTTCTTCATCATCCTGACAATCGATAGGTACCTGGCT 626	A; Resi	cule type: mRNA dues: 1-106,'N',1
	renoily reductions and contraction of the contracti	A;Cros	s-references: GB: : the translated
. T	0.2. GLCGLCCATGCTGTGCTTTAAAAGCCAGGGCGGCTCTTGGGGTGGTGAAATT 686 135 II:1	C;Gene A;Gene	tics: : GDB:CMKBR3
0y 6	GTGATCACTTGGGTGGTGGTTTGCGTCTCCCCAGGAATCATCTTTACCAGAATCT	A; Map	position: 3p21-3p rfamily: vertebra
		C; Keyw F; 36-6	ords: G protein-c 0/Domain: transme
7 7 dg	747 CABABAGAAGGICITACATIACACCIGCAGGICTCAITTTCCAIAC791	F;71-9 F;108- F;147-	F;71-91/Domain: transmer F;108-129/Domain: transm F;147-171/Domain: transm
	dinii paturusiin nisalijinicysserrroniskneriolyrlysserleulysgin	F;205- F;240-	223/Domain: trans 261/Domain: trans
	794 195 TrpLysArgPheGlnAlaLeu-LysLeuAsnLeuCalleleuFolleuLeuFoll	F;288- F;24-2 F;345/	305/Domain: trans 73,106-183/Disulf Binding site: pho
Qy 8	834 CAIGGICAICTGCTACTCGGGAAICCTAAAAACTCTGCTTCGGTGTCGAAAIGAGAAA 893	Alignm	Alignment Scores:
Dp 5	214 lMetileIleCysTyrAlaGlylleIleArglleLeuLeuArgArgProSerGluLy 233	Score:	NO.:
		Fercent Simi Best Local S Ouerv Match:	Fercent Similarity: Best Local Similarity: Query Match:
		DB:	
6	954 TCCCTACAACATTGTCCTTCTCCTGAACACCTTCCAGGAATTCTTTGGCCTGAATAATTG 1013	-60-Sn	
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cabrate rhodopsin
in-coupled receptor; glycoprotein; phosphoprotein; transmembrane p
in-coupled receptor; glycoprotein; phosphoprotein; transmembrane
insmembrane #status predicted <TM1>
ransmembrane #status predicted <TM3>
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ransmembrane #status predicted <TM6>
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sulfide bonds: #status predicted <TM7>
sulfide bonds: #status predicted
predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BL:U49727; NID:91477560; PIDN:AAB09726.1; PID:91477561
40.11649, 1995
unctional expression of a human eosinophil CC chemokine recepto 7237; MUID:95348056; PMID:7622448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108-275,'S',277-280,'R',282-355 <COM>:UZ8694; NID:g1199579; PIDN:AAC50469.1; PID:g1199580 sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC504
                                                PCCAAAAGCACATTGCCAAACGCTTCTGCAAATGCTGTTCTATTTTCCAGCA 1193
                                                                                                                                           CGAGCGAGCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAGGAAATATC 1253
                                                                              |||||:::|||:::|||
heGlnArgHisValAlaIleProLeuAlaLysTrpLeuProPheLeuSerVa 333
                                                                                                                                                                       |||||| ||||||:::||
euGluArgThrSerSerIle---SerProSerThrGlyGluH1sGluLeuSe 352
11AsnProllelleTyrValPheValGlyGluArgPheTrpLysTyrLeuAr 313
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Matches:
Conservative:
Mismatches:
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Gaps:
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1272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence not shown
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CKR-3
is (man)
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70.878
52.858
34.598
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A; Molecule type: mRNA A; Residues: 1-360 < Popy A; Cross-references: GB: X85740; NID: g1370103; PIDN: CAA59743.1; PID: g971452 A; Orde: source clone K5-5 A; Genetics: C; Genetics: A; Gen	Alignment Scores: 1.72e-70	471 471 471 87 87 531 107	Db 127 PheValMetLeuMetSerileAspArgTyrLeuAlaileValHisAlaValPheSeriel 146 Qy 651 AAAGCCAGGACGACGATGGGTGACAAGTGACACTGGTGGTGGTGGTTGGT
AGGCTGAAGAGCATGACCTGCTCAACCTGGCCATCTCTGACCTGTTTTC 476 ATGLEUATGILEMETThASNILETYTLEULEUASNILEUALAILSESETASPLEULEUPHE 83 CTTCTTACTGTCCCCTTCTGGGCTCACTACCTGCCCCCAGTGGGACTTTTCTC 476 [::: :::	104 ALBALBLEUPROGLUPHELLEPHETYGLUTHIGLUGLUGLUCHPHEGLUGLUTHILEUCYS 183 774 AGCTCT	09 1041 TATGCAGGTGACAGAGATGACGCACTGCGCATCAACCCCATCATCTATGC 1100	RESULT 8 A57160 chemokine (C-C) receptor 4 - human N.Alternate names: C-C CKR-4 C;Species: Homo sapiens (man) C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000 C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000 C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000 R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; N.J.; Biol. Cham. 270, 1995 A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor cl A;Reference number: A57160; MUID:95370289; PMID:7642634 A;Reterence number: A57160; MCID:95370289; PMID:7642634 A;Status: preliminary; not compared with conceptual translation

A 375 GTGGGCAACATGCTGATCCTGATAAACTGCAAAAGGCTGAAGAGCATGACT 434	615 AGGTACCTGGCTGCTGCTGTGTTGCTTTAAAAGCCAGGACGGCGCTGGGGGTACCTTGGGGGTACCTGGCTGCTGTGTTGCTTTAAAAGCCAGGACGGCGCCCTTGGGGGTGGTTGCTTTAAAAGCCAGGACGGCCGTTTGGGGACGCTCGCT	, in the second	TOAACCCATCATCTATGCGGGGGAGAGTTCAGAAA : :::	RESULT 10 \$55594 G protein-coupled receptor E1 - equine herpesvirus 2 C;Species: equine herpesvirus 2 C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999 C;Accession: \$55594 E;Accession: \$55594 B;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J. J. Mol. Blol. 249, 520-528, 1995
801 206 861 226 921 245 981	0y 1041 TATGAGGTGACAGACACTTGGGATGACGCACTGCTGCATCATATGC 1100	RESULT 9 JUGASEL 194 INSERDENTITURGINSERTHINGHEASPHISASPLEU 356 RESULT 9 JUGASET 9 JUGASET 196 JUGASET 9 JUGASET 196 JUGASET 9 JUGASET 196	C; Superfamily: vertebrate rhodopsin C; Superfamily: vertebrate rhodopsin C; Superfamily: vertebrate rhodopsin C; Superfamily: vertebrate rhodopsin C; Keywords: glycoprotein; phosphoprotein; receptor; thymus F; 72, 202, 350, Painding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted F; 72, 202, 350, Painding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted F; 72, 202, 350, Painding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted F; 321, Painding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted Alignment Scores: Covalent) (by protein kinase C) #status predicted Alignment Scores: Score: Score: Score: Covalent) (by protein kinase C) #status predicted Alignment Scores: Score: Sc	OY 264 ATCTATGATTATTAT =ACATCGGAGCCCTGCCAAAAATGTG 314 ::: ::: ::: ::: :::

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MIP-1 alpha receptor like-1 - mouse
C;Species: Max musculus (house mouse)
C;Species: Max musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: 149340
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17444-17501, 1995
A;Title: Clouming and differential tissue-specific expression of three mouse beta chem A;Reference number: 149339; MUID:95340546; PMID:7542241
A;Accession: 149340
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                        1071 GCACTGCTGCATCAACCCCATCATGTATGCCTTTGTCGGGGAGAAGTTCAGAAACTACCT 1130
                                                                                                                             1131 CTTAGTCTTCTTCCAAAAGCACATTGCCAAACGCTTCTGCAAATGCTGTTCTATTTTCCA 1190
                                                                                300 CAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG 359
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nCysalaLeuSerSerAsnLeuAspMetAlaLeuIeuIleThrIysThrValAlaTyrTh 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-356 (KERS)
A; Cross references: EMEL:1284(05; NID:9881549; PIDN:AAA89154.1; PID:9881550
C; Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 ValThrGluProSerTyrAsnThrValAlaLysAsnAspPheMetSerGlyPheLeuCys
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158
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110
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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Pred. No.:
                         311
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ValVallielleVallileArgTyrMetLys1leLysAsnLeuThrAsnMetLeuLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 GlyMetTyrHisAspTrpThrPheGlylleSerLeuCysLysLeuLeuArgGlyValCys 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||| |||||| :::||| CysValCysThrTrpPheLeualaGlyLeuLeuSerLeuProGluPhePhePheHisGly 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HisGlnAspAspAsnGlyArgValGlnCysAspProTyrTyrPro-GluMetSerThrAs 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGAGGCACAGGGCTGTGAGGCTTATCTTCACCATCATGATTGTTTATTTTCTCTTCTG 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            390 GICAICCICATCCIGATAAACIGCAAAAGGCIGAAGAGCAIGACIGACAICTACCIGCIC 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   510 GCCGCC-----CAGIGGGACTTTGGAAATACAATGTGTCAACTCTTGACAGGGCTCTAT 563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                450 AACCIGGCCAICICIGACCIGIITITICCITCITACIGICCCCITCIGGGCICACIAIGCT 509
                                                                                                                                                                                                                                                                                                                                                                              291 pThrProTyrAsnIleValLeuLeuLeuSerThrPheHisAlaThrLeuLeuAsnLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 TCTCAAAAAGAAGGTCTTCATTACACCTGCAGGTCTCATTTTCCATACATTA------
                                                                                                      A;Cross-references: GB:U20824; NID:g695172; PIDN:AAC1378B.1; PID:g695173 C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor
                                                                                                                                                                                             383
156
64
92
20
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MUID:95302501; PMID:7783207
A;Accession: S55594
                                                      A; Status: preliminary; nucleic acid sequence not shown
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Matches:
Conservative:
Mismatches:
Indels:
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Query Match:
                                                                                       A; Residues: 1-383 <TEL>
                                                                     A; Molecule type: DNA
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셤 δ g Qγ 셤 δ g δ g Q g Q ď δ 셤 δ 셤 ð 셤

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C;Genetics: A;Gene: GDB:CMKBRB; CMKBRL2; TER1; CKR-L1 A;CrOSs-references: GDB:6053733; OMIN:601834 A;Map position: 3p21-3p21 C;Superfamily: vertebrate rhodopsin C;Keywords: G protein-coupled receptor; transmembrane protein F;36-63/Domain: transmembrane #status predicted <tml> F;73-94/Domain: transmembrane #status predicted <tml> F;108-129/Domain: transmembrane #status predicted <tml> F;200-222/Domain: transmembrane #status predicted <tma> F;200-222/Domain: transmembrane #status predicted <tma> F;201-260/Domain: transmembrane #status predicted <tma> F;201-260/Domain: transmembrane #status predicted <tma> F;201-20/Domain: transmembrane #status predicted <tma> F;201-20/Domain: transmembrane #status predicted <tma> F;201-304/Domain: transmembrane #status predicted <tma></tma></tma></tma></tma></tma></tma></tma></tml></tml></tml>	Alignment Scores: 5.43e-55 Length: 355 Pred. No.: 716.00 Matches: 144 Percent Similarity: 59.28 Conservative: 71 Best Local Similarity: 40.00% Mismatches: 114 Query Match: 27.25% Indels: 31 DB: 2 Gaps: 7 US-09-938-703-3 (1-1442) x JC5067 (1-355)	Qy 240 AIGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTAT 284		Qy 405 ATAAACTGCAAAAGGCTGAAGATGACTGACTGACTGCTCAACCTGGCCATCTCT 464 ::: :::	QY 465 GACCTGTTTTCCTTACTCCCCTTCTGGCCTCACTAGCTGCCGCCCAGTGGAC 524		645	QY 705 GCTGTGTTTGCGTCTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAGGTCTT 761 ::: ::: ::::	QY 762 CAIT	QY 795 AAAGATAGTCATCTTGGGGCTGCTGCTGCTGCTGTGATGGTCATCTGCTACTCGGG 854	Qy 855 AATCCTAAAAACTCTGCTGTGTCGAAATGAGAAGAGGGCACAGGCTGTGAGGCT 914	QY 915 TATCTTCACCATCATGATTGTTTATTTTCTCTTCTGGGCTCCCTACACATTGTCCTTCT 974
	225 225 244 984 264	GCAGGTGACAGAGACTCTTGGGATGACGACTGCTGACCCCATCACCTTGTGCCTT :::	Dy evaluations of the control of the		RESULT 12 UC5067 G protein-coupled receptor CKR-L1 - human N.Alternate names: chemokine receptor-like protein TER1; GPR-CY6 C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Sate: 31-Jan-1997 *sequence_revision 31-Jan-1997 *text change 21-Jul-2000	; G02776; G02387 'Ona, R.; Gutierrez, J.; Lind, P.; Marquez, G. tes. Commun. 227, 846-853, 1996 COOLING and RNA expression of two new human chemoki JC5067; MUID:97040707; PMID:8886020	2.1; PID:91668736	submitted to the EMBL Data Library, June 1996 A; Reference number: H01714 A; Accession: G02776	A.Status: translated from GB/EMBL/DDBJ A.Molecule type: DNA A.Residues: 1.355 < NAP> A.Tessidues: 1.355 < NAP> A.Cross-references: EMBL:U62556; NID:q1468978; PID:q1468979	R.Bonner, T.I. submitted to the EMBL Data Library, January 1996 A.Reference number: H01154 A.Accession: G02387	A.Status: preliminary; translated from GB/EMBL/DDBJ A.Molecule type: DNA A.Residues: 1-355 <bon> A.Cross-references: EMBL: U45983; NID:q1245056; PID:q1245057</bon>	C; Comment: This protein belongs to the family of beta chemokine receptors.

us-09-938-703-3.rpr

Db 104 LysleuthrthralaPhePhePhelleGlyPhePheClyGlyIlePhePheIlethrval 1233 Qy 11eSerileAspargTyTeualaleGevertion	SULT 14 4304 phan G prote phan G prote Alternate no Species: Hon Species: Hon Species: Hon Species: Hon Species: Hon Species: Hon Report, C.J Report, C.J Report, C.J Report, C.J Report Species: Hon Residues: I Stoos-refere Comment: Thi Comment: Thi Species: The Species: Hon Spe
Db 239 UVALLEURIPATIONAL PROPERTY	US-09-938-703-3 (1-1442) x 158186 (1-354) QY

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|HisAanAlaMetCysLysPheThrThrAlaPhePhePheIleGlyPhePheGlySerIle 117
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TyrSerValllePheAlaIleGlyLeuValGlyAsnLeuLeuValValPheAlaIeuThr 57
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18 AlaGluAlaCysTyrIleGlyAspileValValPheGlyThrValPheLeuSerIlePhe
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F;35-57/Domain: transmembrane #status predicted <TM1>
F;66-88/Domain: transmembrane #status predicted <TM2>
F;104-125/Domain: transmembrane #status predicted <TM3+
F;146-165/Domain: transmembrane #status predicted <TM4+
F;197-17/Domain: transmembrane #status predicted <TM4+
F;197-17/Domain: transmembrane #status predicted <TM5+
F;230-254/Domain: transmembrane #status predicted <TM5-
F;275-296/Domain: transmembrane #status predicted <TM5-
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Matches:
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1095 CTATGCCTTTGTCGGGGAGAGTTCAGAAACTACCTCTTAGTCTTCTTCCAAAAGCACAT 1154
              292 eTyrAlaPheAlaGlyGluLysPheArgArgTyrLeuTyrHisLeuTyrGlyLysCysLe 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TACTCACTGGTGTTCATCTTTGGTTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATA 407
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|159 AlaileLeuAlaThrLeuProGluTyrValValTyrIysProGlnMetGluAspGlnLys 178
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                                                                                                                                                                       C; Species: Homo sapiens (man)
C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C; Accession Jul-399 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C; Accession Jul-399 #sequence_revision 16-Jul-1999
Blochem. Blophys. Res. Commun. 243, 264-268, 1998
A; Hitle: Cloning and characterization of a novel human chemokine receptor.
A; Reference number: JC5942; MUID:98139902; PMID:9473515
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288 TCGGAGCCTGCCAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCGGCTC
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PhePheAsnCysLeuLeuThrYalGlnArgTyrLeuValPheLeuHisLysGlyAsnPhe
                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:U97123; NID:92897070; PIDN:AAC39595.1; PID:92897071
C;Superfamily: vertebrate rhodopsin
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1083 CAACCCCATCATCTATGCCTTTGTCGGGAGAAGTTCAGAAACTACCTCTTAGTCTTCTT 1142
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                                                                   903 GGCTGTGAGGCTTATCTTCACCATCATGATTGTTTATTTTCTTTGGGCTCCCTACAA 962
                                                                                 235 rLeuPheLysLeuValPheAlalleMetValValPheLeuLeuMetTrpAlaProTyrAs 255
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                                           1203 CGAGCGAGCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAGGAA 1248
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Search completed: June 3, 2003, 18:51:41 Job time: 65.6953 secs

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GenCore version 5.1.6
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using frame_plus_n2p model OM nucleic - protein search,

June 3, 2003, 18:39:54; Search time 23.4701 Seconds Run on:

(without alignments)
5096.611 Million cell updates/sec

US-09-938-703-3 2628 Title: Perfect score:

1 GAATTCCCCCAACAGAGCCA......AGTAGATTAGATCCGAATTC 1442

Sequence:

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112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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æ	Query Match	66.4	66.2	0.99	65.8	65.7	65.5	65.5	65.4	65.4	65.4	65.4	65.0	64.5	56.1	56.1	201	0 1	50.5	50.1
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SEQUENCE FROM N.A. MCCOmbie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,

J. Leukoc. Biol. 60:147-152(1996).

7 homo sapien				_													_									
P4159	P32246	P51678	054814	P51675	P56482	P51677	P56483	09221	P51679	P5649	P5168	P51676	P5168	99260	P56484	P3541	600z60	P4923	P51686	P3224	09wnt	P47774	065000	202800	009027	P51684
CKR2 HUMAN	CKR1_HUMAN	CKR3_MOUSE	CKR3_RAT	CKR1_MOUSE	CKR1 MACMU	CKR3 HUMAN	CKR3 MACMU	CKR3 CAVPO	CKR4_HUMAN	CKR3_CERAE	CKR4 MOUSE	CKRV MOUSE	CKR8 HUMAN	CKR8 MACMU	CKR8 MOUSE	C3X1_RAT	C3X1 MOUSE	C3X1_HUMAN	CKR9_HUMAN	CKR7_HUMAN	CKR9 MOUSE	CKR7 MOUSE	CKD6_HUMAN	CKD6_MOUSE	CKD6_RAT	CKR6_HUMAN
7	Н	Н	Н	Н	Н	ч	Н	Н	щ	1	-4	1	М	Н	⊣	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Ч
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45.3	38.2	37.1	37.1	m					33.9	33.6	33.4	29.5	27.2	27.0	27.0	26.2	25.5	•	22.2		21.6	21.2	21.2	21.1	21.1	21.0
1191	1003.5	976	974	950	949.5	912	905	898.5	891.5	884	878.5	176	716	709.5	708.5	688.5	669.5	644	582.5	573.5	566.5	556.5	556.5	555	554	552.5
19	20	21	22	23	24	22	56	27	78	29	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

[2]
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P51681; 014692; 014693; 014695; 014697; 014706; 014707; 014707; 014707; 014707; 014707; 014707; 01538; 09DRA;
01-0CT-1996 (Rel. 34, Created)
15-UNN-2002 (Rel. 44, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
C-C-chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR-5) (CCR5)
CCR5 OR CMKBN5. ပ္ပ Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. MCBL_TaxID=5606; MEDLINE-96295970; PubMed-8699119; Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.; "Cloning and functional expression of CC CKR5, a human monocyte chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and [1]
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AF011511;
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-1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLUIAR CALCIUM IONS LEVEL. MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR DIFFERENTIATION. ACTS AS CO-RECEPTOR WITH CD4 FOR PRIMARY NON-SYNCYTUM-INDUCING STRAINS (NSI) (MACROPHAGE-TROPIC) OF HIV-1 VIRUS. IT PROMOTES ENV-MEDIATED FUSION OF THE VIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                        thang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
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Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Murny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.W., Dragan Y., Glacalone J., Pae A., Powell B., Solinsky K.A., Desliva U., Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., Sagripanti J.L.; Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism."; AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
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TISSUE SPECIFICITY: FOUND IN PROMYELOCYTIC CELLS.
PTM: SULFATION CONTRIBUTES TO THE EFFICIENCY OF HIV-1 ENTRY.
PTM: MODIFIED BY O-LINKED GLYCOSYLATION, BUT NOT BY N-LINKED
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MEDLINE-96260017; PubMed-8649511;
Deptg H., Liu R., Ellmeter W., Choe S., Unutmaz D., Burkhart M.,
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Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
"Identification of a major co-receptor for primary isolates of
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MEDLINE-96260018; PubMed-8649512;
Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,
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Nature 381:667-673(1996).
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
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AF011500; AAB65700.1; -.
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AAB65735.1; -.
AAB65736.1; -.
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927 240 987 260 1047 280	Db 300 GlyGluLysPheArgAsnTyrLeuLeuValPhePheGlnLysRislleAlaLysArgPh 320 Qy	£ 5		GN CCR5 OR CMKBR5. OS Pan troglodytes (Chimpanzee). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. OX MCFH TANTD-0508.	Sharron M., Samson M., Lu Z.H. Peiper S.C., Parmentier M., B. Differential utilization of		RA Zimmerman P.A., Buckler-White A., Alkhatib G.; RL Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases. RN [3] RP SEQUENCE FROM M.A.	RX MEDLINE-98022612; PubMed-9359654; RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B., RA Ho D.D.; RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.":		RA Zacharova V., Zachar V., Goustin A.S.; RT "Sequence of Chemokine receptor gene CCRS in chimpanzees, a natural RT HIV type 1 host."; RL AIDS Res. Hum. Retroviruses 13:1159-1161(1997).		RI "Chimperzee CKCR4 and CCR5 act as coreceptors for HIV type 1."; RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997). CC -1- FUNCTION: RECEPTOR ROR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, CC -INCREASING THE INTRACELLUIAR CALCIUM IONS LEVEL. MAY PLAY A ROLE CC INCREASING THE INTRACELLUIAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
FT TRANSMEM 236 260 6 (POTENTIAL). FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL). FT TRANSMEM 278 301 7 (POTENTIAL). FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL). FT DISULFID 101 178 BY SINILARITY. FT MOD_RES 13 3 SULFATION. FT MOD_RES 10 10 SULFATION. FT MOD_RES 15 15 SULFATION. FT WARLANT 10 10 Y -> D (IN INCR5-71A). FT YARIANT 29 29 A -> S (IN DBSNE):1800939). FT YARIANT 31 31 R -> H (IN INCR5-72A).	Alignment Scores: 5.25e-131 Length: 352 Pred. No.: 1745.50 Matches: 340 Percent Similarity: 96.60% Conservative: 1 Pest Local Similarity: 96.32% Mismatches: 0 Query Match: 1 Gaps: 12 DB: 1 Gaps: 1	US-09-938-703-3 (1-1442) x CKR5_HUMAN (1-352) QY 240 AFGGATTATCAAGTGTCAAGTCCAATCTATGACATCAGTGGAGCCCTGC 299 Db 1 MetAaplyrGlnValSerSerPorlleTytablieAsnTyrTyrThrSerGlnPalSerSerPorlleTyrTyrThrSerGlnPalSerSerPorlleTyrTyrThrSerGlnPalSerSerPorlleTyrTyrThrSerGlnValSerSerPorlleTyrThrSerGlnValSerSerPorlleTyrTyrThrSerGlnValSerSerPorlleTyrThrSerGlnValSerSerPorlleTyrThrSerGlnValSerSerPorlleTyrThrSerGlnValSerSerPorlleTyrThrSerGlnValSerSerPorlleTyrThrSerGlnValSerSerPorlleTyrThrSerGlnValSerSerPorlleTyrThrSerGlnValSerSerPorlleTyrThrSerGlnValSerSerPorlleTyrThrSerGlnValSerSerPorlleTyrThrSerGlnValSerSerPorlleTyrThrSerGlnValSerSerPorlleTyrThrSerGlnValSerSerPorlleTyrThrSerGlnValSerSerPorlleTyrThrSerGlnValSerSerPorlleTyrThrSerGlnValSerSerPorlleTyrThrSerGlnValSerSerPorlleTyrThrSerGlnValSerSerPorlleTyrThrSerGlnValSerSerPorlleTyrThrSerGlnValSerPorlleTyrThrSerGlnValSerSer	Oy 300 CAAAAAATCAATGTGAAGCAAATGGCAGCCCGCCTCCTGCCTCTACTCACTC	Qy 360 TICATCTITGGTTITGTGGGCAACAIGCTGGTCATCCTCATCCTGATAACTGCAAAGG 419 	QY 480 CTRACTGTCCCTTCTGGGCTCACTACTGCCCCCCAGTGGGACTTTGGAAATACAATG 539 DD	OY 540 TGTCAACTCTTGACAGGCTCTATTTATAGGCTICTTCTCTGGAATCTTCTTCATCATC 599	QY 600 CTCCTGACAATCGATACCTGGCTGTCCATGCTGTGTTTGCTTTAAAAGCCAGG 659	OY 660 ACGGTCACCTTGGGGTGACAAGTGTGATCACTTGGGTGGTGGTGTGTTTGCGTCT 119	Qy 720 CICCCAGGAAICAICITIACCAGAICTCAAAAAGAAGGICTICATIACACCIGCAGCTCI 779 	OY 780 CATITICCATAC	Qy 807 CTTGGGGCTGGTCGCCGCTGGTTGTCATGGTCATCTTGCTACTCGGGAATCCTAAAAAC 866 DD 111111111111111111111111111111111111	Oy 867 TCTGCTTCGGTGTCGAAATGAGAAGAGGCACAGGGCTGTGAGGCTTATCTTCACCAT 926

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1107 CGGGGAGAAGTTCAGAAACTACCTCTTAGTCTTCTTCCAAAAGCACATTGCCAAACGCTT 1166
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     LeuLysSerMetThrAspIleTyrLeuLeuAsnLeuAlaIleSerAspLeuPhePheLeu
                                                      CTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCCAGTGGGACTTTGGAAATACAATG
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30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2012 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
CCR5 OR CMKRR5.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pongo.
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SEQUENCE FROM N.A.
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                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pfan; PP00001; 7tm_1; 1.
PRINTS; PP000037; G_PROTEIN_RECEP_FI_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_FI_2; 1.
PROSITE; PS002062; G_PROTEIN_RECEP_FI_2; 1.
PROSITE; PS002062; G_PROTEIN_RECEP_FI_2; 1.
G_PROTEIN COUPLED TRANSMEMBRANES: GIYCOPTOTEIN; Sulfation.
G_PROTEIN (POTENTIAL).
                                              SUBCELLUTAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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THE CONTROL OF GRANDLOCYTIC LINEAGE PROLIFERATION OR
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InterPro; IPR000276; GPCR_Rhodpsn.
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15-JUL-1998 (Rel. 36, Last sequence update)
16-GCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
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                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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             Zhang Y.-W., Ryder O.A., Zhang Y.-P.,
"Sequence evolution of the CCR5 chemokine receptor gene in primates.",
Mol. Biol. Evol. 16:1145-1154(1999).
--I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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PRINTS; PR00237; GPCRHODDPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G_protein coupled receptor; Transmembrane; Glycoprotein; DOMAIN
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SULFATION
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InterPro; IPR000276; GPCR_Rhodpsn.
   MEDLINE-99416438; PubMed-10486970;
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Trachypithecus phayrei (Phayre's leaf monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
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15-JUN-2002 [Rel. 41, Last annotation update)
C-C chemokine_receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
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Proc. Natl. Acad. Sci. U.S.A. 94.4005-4010(1997).
--I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BIDDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEYEL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
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PRIMTS; PR00027; GPCR_Rhodpsn.
PROSITE; PS00237; GPCRRHODOPSN.
PROSITE; PS00237; G_RROTEIN_RECEP_FI_1; 1.
G-protein coupled receptor; Transmenbrane; Glycoprotein; Sulfation.
DOMAIN 1 59 EXTRACELLUIAR (POTENTIAL).
TRANSMEM 59 68 CYTOPIASMIC (POTENTIAL).
TRANSMEM 69 89 2 (POTENTIAL).
                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M., Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M., Petiper S.C., Parmentier M., Broder C.C., Doms R.W.; Priferential utilization of CCR5 by macrophage and T cell tropic
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                                                                                 CITACTGTCCCCTTCTGGGCTCACTATGCTGCCCCCAGTGGGACTTTGGAAATACAATG 539
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15-JUL-1998 (Rel. 36, Last sequence update)
16-JUL-1998 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5).
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Papio anubis (Olive baboon).
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                                                                                                                           FUNCTION: RECEPTOR FOR C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, FUNCTION: RECEPTOR FAND SUBSEQUENTLY TRANSDUCES A SIGNAL BY MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL, MAY PLAY A ROLE INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL, MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
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PRINTS; PR00237; GPRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS02023; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS02024; G_PROTEIN_RECEP_F1_2; 1.
STOTE OUTLOOK COORDING TRANSMEMBRANCE; Glycoprotein; Sulfation.
DOMAIN
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InterPro; IPR000276; GPCR_Rhodpsn.
                                                               SEQUENCE FROM N.A.
MEDLINE=99416438; PubMed=10486970;
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NCBL_TaxID=61618;
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                                                                                                                                                                                                                                                                                                             SPECIES-P.hamadryas, MEDLINB-99210133; PubMed=10195758; Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.; "Species-specific changes in the CCR5 gene from African and Aslan nonhuman primates."
                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLUAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Pfam; PF00001; 7tm_1; 1.
PRINES; PR00237; GPRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_ECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_ERCEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN 1 30 EXTRACELLOIAR (POTENTIAL).
                                                                       SPECIES-P.hamadryas,
MEDLINE-97268687; PubMed-9108095;
Rdinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
"Differential utilization of CCR5 by macrophage and T cell tropic
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Frimates; Catarrhini; Cercopithecidae;
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Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
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EMBL; AF105288; AAD20557.1;
EMBL; AF105289; AAD20557.1;
EMBL; AF105290; AAD20559.1;
EMBL; AF023452; AAC63830.1;
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                         Cercopithecinae; Papio.
                                       NCBI_TaxID=9557, 9555;
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Matches:
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Best Local Similarity:
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                        1107 CGGGGAGAAGTICAGAAACTACCICITAGICTICCIAAAAGCACATIGCCAAAACGCTI 1166
                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mode in a non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
                                        280 nValThrGluThrLeuGlyMetThrHisCysCysIleAsnProIleILeTyrAlaPheVa 300
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99416438; PubMed=10486970; Zhang Y.-P.; Zhang Y.-P.; Ryder O.A., Zhang Y.-P.; Squence evolution of the CCR5 chemokine receptor gene in primates."; Mol. Biol. Evol. 16:1045-1154(1999).

-I FUNCTION; RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, MIP-1-BETA AND RAWITES AND SUBSEQUENTLY TRANSPORCES A SIGNAL BY INCREASING THE INTRACELLUIAN CALCIUM IONS LEFEL, MAY PLAY A ROLE IN THE COMPTOL, OF GRANULOCYTIC LINEAGE PROLIFERATION OR
                                                                                                                                                                                                                                                                                     Trachypithecus francoisi (Francois' langur) (Indochinese langur).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
C-C_chemokine_receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5).
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Interpro: IPRO0276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm.1: 1.
PRINTS; PR00237; G_PCRHODOPSN.
PROSITE; PS00237; G_PROTEIN RECEP_F1.1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1.2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
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EXTRACELLUIAR (POTENTIAL).
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SEQUENCE FROM N.A.

**MEDLINE-9941648 19: PubMed-10486970;
Zhang Y.-W., Zhang Y.-P.;

**Sequence evolution of the CCR5 chemokine receptor gene in primates.";

**Mol. Brol. 16:1145-1154(1999).

**INTELL BRIA AND RAWINES AND SUBBEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRREACELLUIAR CALCIUM IONS LEVEL. MAY PLAY A ROLE IN THE COMPROL OF GRANULOCYTIC LINEAGE PROLIEFRATION OR

DIFFERENTIATION.
                                                                                                                                                                                                                                                                                                                                                                                         Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae, Colobinae,
                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
C-C chemokine_receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1: 1.
PRINTS; PR0027; GPCRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
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CYTOPLASMIC (POTENTIAL),
2 (POTENTIAL),
EXTRACELLULAR (POTENTIAL)
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GGIGACAGAGACTCTTGGGATGACGCACTGCTGCATCAACCCCCATCATCTATGCCTTTGT 1106
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Zhang Y.-W., RgAder O.A., Zhang Y.-P.;
"Sequence evolution of the CCR5 chemokine receptor gene in primates.";
Mol. Biol. Evol. 16:1145-1154(1999).
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-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE IN THE CONTROL. OF GRANDLOCYTIC LINEAGE PROLIFERATION OR
                                                                                                                                                                                                                                                                                                                                                                                                    Pygathrix nemaeus (Dove langur).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
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InterPro; IPR000276; GPCR_Rhodpsn.
PRIME; PR00001; 7tm 1; 1.
PROSITE; P800237; GPROTEIN_RECEP_F1_1; 1.
PROSITE; P8500237; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
EXTREMEDIATE PAGENTIAL: 30
EXTREMENTAL: ACTUALIZED SULFATION.
                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CRR-5) (CCR-5) (CCR5).
CCR5 OR CMEBR5.
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Percent Similarity:
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                                                                                                 CGGGGAGAAGTTCAGAAACTACTCTTAGTCTTCCAAAAGCACATTGCCAAACGCTT 1166
                                                                                                                                                                                MEDLINE-99416438; PubMed-10486970;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Sequence evolution of the CCR5 chemokine receptor gene in primates.";
Mol. Biol., Evol. 16:1145-1154(1999).
-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
                                                                                                                        or send an emc...

EMBL, AF075451; AA019663.1; -.

InterPro; IPR000276; GPCR_Rhodpsn.

Profan; PR000017; Trm.1; 1.

PRINTS; PR000237; G_PROTEIN_RECEP_FL_1; 1.

PROSITE; PS00267; G_PROTEIN_RECEP_FL_1; 1.

PROSITE; PROSITE; PROSITE; PROTEIN_RECEP_FL_1; 1.

PROSITE; PROSITE; PROSITE; PROSITE PROSITE; PROSITE PRO
                      .047 GGTGACAGAGACTCTTGGGATGACGCACTGCTGCATCAACCCCATCATCTATGCTTTGT
                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
BY SIMLARITY.
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SULFATION (BY SIMILARITY)
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Indels:
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Matches:
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                                                                           40445 MW;
                                                                                                         7.3e-129
1718.50
95.75%
94.62%
65.39%
                                15
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                                                                         352 AA;
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SUBCELLULAR LOCATION: Integral membrane protein
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EMBL; AF005661; AAB62555.1; -..
EMBL; AF005662; AAB62556.1; -..
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                                                                                                                                                        GGTGACAGAGACTCTTGGGATGACGCACTGCTGCATCAACCCCATCATCTATGCCTTTGT 1106
                                                                                                                                                                               SPECIES-M.milatta, M.fascicularis, and M.nemestrina;
MEDLINE-97268687: PubMed-9108095;
Bedinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
Pelper S.C., Parmentier M., Broder C.C., Doms R.W.;
"Differential utilization of CCR5 by macrophage and T cell tropic
simian immunodeficiency virus strains.";
Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
-: FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEYBL. MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR DIFFERENTIATION.
                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CRR-5) (CCR-5) (CCR-5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES—M.mulatta; STRAIN-Indian macaque; MEDLINE-97213934; PubMed-9060623; Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.; "Genetically divergent strains of simian immunodeficiency virus use CCR5 as a coreceptor for entry."; J. Virol. 71:2705-2714(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and Macaca nemestrina (Pig-Talled macaque). Elikaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Margulies B.J., Hauer D.A., Clements J.E.; Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES-M.mulatta;
Marbine-D7184592; PubMed-9032394;
Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
Newman W., Gerard N., Gerard C., Sodroski J.;
(Tillization of C-C chemokine receptor 5 by the envelope
glycoproteins of a pathogenic simian immunodeficiency virus,
SIYMmac199.";
                                                                                                                                                                                                                                       CCGATCCACTGGGGAGCAGGAAATATCTGTGGGCTTG 1263
                                                                                                                                                                                                                                                            receptors.";
AIDS Res. Hum. Retroviruses 17:981-986(2001).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PRINTS; PR00027; GPCRENOGPSN.
PROSITE; PS00237; GPROTEIN_RECEP_FI_1; 1.
PROSITE; PS50263; G_PROTEIN_RECEP_FI_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN 1 30 EXTRACELLUIAR (POTENTIAL).
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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N- I (IN REF. 3).

I -> M (IN REF. 3).

SBB96CB590FRCB2 CRC64;
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BY SIMILARITY.
SULPATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
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us-09-938-703-3.rsp

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US-09-938-703-3 (1-1442) x CKR5_CERTO (1-352)
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                                                                      CICCTGACAATCGATAGGTACCTGGCTGTCGTCCATGCTGTGTTTGCTTTAAAAGCCAGG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGATCCACTGGGGAGCAGGAAATATCTGTGGGCTTG 1263
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352 AA.
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SEQUENCE FROM N.A.
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                              Chen Z., Gettie A., Ho D.D., Marx P.A.;

"Primary Siysm isolates use the CCR5 coreceptor from sooty mangabeys naturally infected in west Africa: a comparison of coreceptor usage of primary Siysm, HIV-2, and Siymac.";

Virology 246:113-124(1998).

-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEWOKINE. BINDS TO MIP-1-ALPHA, MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLURAR CALCIUM IONS LEYEL. MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; Lr., Tm_1; 1.
Print's Pr00001; Tm_1; 1.
PRINTS: PR00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50252; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50252; G_PROTEIN_RECEP_F1_2; 1.
EXTRACELLOLAR (POTENTIAL).

SATRACELLOLAR (POTENTIAL).
                                                                                                                                                                                                           SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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D -> E (IN ISOLATE 087).
Y -> D (IN ISOLATE 087).
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STRAIN=Isolate 079, 085, 087, and 089;
MEDLINE=98321155; Pubmed=9656999;
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                                                                                                                                                                                                                                                                                                                                                                       SUBMITTED (JUL-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTY TRANSDORES A SIGNL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEYEL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
                                          JUL-1998 (Rel. 36, Last sequence update)
OCT-2001 (Rel. 40, Last annotation update)
chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR-5).
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                                                                                              Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                           Kuhmann S.E., Platt E.T., Kozak S.L., Kabat D.; "Polymorphisms in the CCR5 genes of African green monkeys and micliplicate specific annion acids in infections by simian and human immunodeficiency viruses."; Virol. 71:8642-8656(1997).
                                                                                                                                                                                                                                                                                                                                 Murayama Y., Matsunaga S., Inoue-Murayama M.;
"CDNA sequence of African green monkey CCR-5 chemokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00237; GPCRHHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP_F1_1; 1.
PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
G_PTOTE: Coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
1 30 EXTRACELLULAR (POTENTIAL).
TRANSMEM 31 58 1 (POTENTIAL).
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EXTRACELUTAR (POTENTIAL).

5 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                 TISSUE=Kidney;
MEDLINE~98001387; PubMed=9343222;
                                                                                                                                             Cercopithecinae; Cercopithecus.
                              (Rel. 36, Created)
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                                                                                                                                                          NCBI_TaxID=9534;
                                                                                    CCR5 OR CMKBR5.
                           15-JUL-1998
                                                         16-0CT-2001
CKR5_CERAE
P56493;
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                                                      CGGGGGAGAAGTICAGAACTACCTCTTAGTCTTCTTCCAAAAGCACATTGCCAAACGCTT
                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                         STRAIN-Wister; TISSUE-Brain; MEDLINE-98334064; PubMed-9670989; Spleists O., Gourmala N., Boddeke H.W.G.M., Sauter A., Flebich B.L., Berger M., Gebicke-Haerter P.J.; "Cloning of rat HIV-1-chemokine coreceptor CKR5 from microglia and upregulation of its mRNA in ischemic and endotoxinemic rat brain.";
                                                                                                                                                                                          NOV-1997 (Rel. 35, Last sequence update)
4AY-2000 (Rel. 39, Last annotation update)
chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (MIP-1
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3 (POTENTIAL).
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2 (POTENTIAL).
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SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley;
MEDLINE-98318173; PubMed-9655467;
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                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                             STANDARD;
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                                                                               260 rThrPheGlnGluIYrPheGlyLeuAsnAsnCysSerSerSerAsnArgLeuAspGlnAl
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lalpha receptors: evidence for two closely linked C-C chemokine
receptors on chromosome 9.";
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P51682, Q61867, P97405, O35313; P97308; O35891;
01-0CT-1996 (Rel. 34, Created)
15--UT-1998 (Rel. 36, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (MIP-1)
A part of the completion of the comp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.; "Cloning and characterization of a novel murine macrophage inflammatory protein-1 alpha receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTACACCCGATCCACTGGGGAGCAGGAAATATCTGTGGGCTTG 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE FROM N.A.
STRAIN-CS7BL/6 X CBA: TISSUB-Thymus;
STRAIN-C57BL/6 X CBA: TISSUB-Thymus;
MEDLINE-96278910; Pubmed-8662890;
MCDLINE-96278910; Pubmed-8662890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem. 271:14445-14451(1996)
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Biol. Chem. 271:7551-7558(1996).
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STRAIN-129;
MEDLINE-97404635; PubMed-9261347;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=129/SvJ; TISSUE=Spleen; MEDLINE=96205938; PubMed=86317
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SEQUENCE FROM N.A.
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PRINTS; PROUGO1; 7tm_1; 1.
PRINTS; PROUGO1; 7tm_1; 1.
PROSITE; PSU0237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.
FIGURE COUPLED TO STREEP F1_2; 1.
FIGURE COUPLED TO STREEP F1_1; 1.
FIGURE COUPLE TO STREEP F1_1; 1.
FIGURE
                                                                                                     GLO B., Kuno K., Harada A., Matsushima K.;
Submitted (JAN-1997) to the EMBL/Genbank/DDBJ databases.
-- FUNCTION: RECEPTOR FOR A C.-C TYPE CHRANKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BERA AND RANDES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
-- SUBCRELULAR LOCATION: Integral membrane protein.
-- TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CELL LINES,
BUT NOT IN NONHEMATOPOLETIC CELL LINES.
-- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H., Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.; "Two distinct CCRS domains can mediate coreceptor usage by human immunodeficiency virus type 1.";
J. virol. 71:6305-6314(1997).
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S (IN REF. 1).
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EMBL; U68565; AAB37273.1; -.
EMBL; U83327; AAC53386.1; -.
EMBL; AP022990; AAC53389.1; -.
EMBL; AP019772; AAB71183.1; -.
EMBL; D83648; BAA12024.1; -.
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|SerProHisPheProHisThrGlnTyrHisPheTrpLysSerPheGlnThrLeu-IysMe 200
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300 aPheValGlyGluLysPheArgSerTyrLeuSerValPhePheArgLysHisIleValLy 320
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120	.220	140
300 aPheValGlyGluLysPheArgSerTyrLeuSerValPhePheArgLysHisIleValLy 320	1161 ACGCTTCTGCAAATGCTGTTCTATTTTCCAGCAAGAGGCTCCCGAGCGAG	320 sArgPheCysLysArgCysSerIlePheGlnGlnAspAsnProAspArgValSerSerVa 340
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³²⁰ sArgPheCysLysArgCysSerIlePheGlnGlnAspAsnProAspArgValSerSerVa 340

Search completed: June 3, 2003, 18:46:01 Job time: 39.4701 secs

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Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
NCBL_TaxID-9590;
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Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF1/7984; AAK43367.1;
-1 InterPro; IPR000276; GPCR_Rhodpsn.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
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         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                          using frame_plus_n2p model
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Maximum Match 100%
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Ygapop 10.0 , Ygapext C
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01-JAN-1998 (TIEMBLIEL. 05, Last sequence update)
01-DEC-2001 (TIEMBLIEL. 19, Last annotation update)
0CR5 receptor (Fragment).
CR5.
Pan troglodytes (Chimpanzee).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                            C STRAIN-GECCR5-141...;
A zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn Ho.D.;
A D.D.;
T ulty-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
T alds Res. Hum. Retroviruses 0:0-0(1997).
EMBL; AF011539; AAB65739.1; -.
InterPro; IPP000276; GPCR_Rhodpsn.
DR PRIM: PF000137; GPCR_Rhodpsn.
DR PRIMIS; PR00237; GPCR_RHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
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352 AA; 40466 MW; 3FFFAC7ABAE1D4FB CRC64;
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F4F64B3AD5AF658A CRC64;
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                                                                                                 US-09-938-703-3 (1-1442) x Q95NC5 (1-352)
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          PROSITE; PS00237; G_PROTEIN_RECEP_FI_1; PROSITE; PS50262; G_PROTEIN_RECEP_FI_2;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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SENGUENCE FROM N.A.
STARIN-CHCCRE-142A;
Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G.,
HD 0.D.;
HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
AIDS Res. Hum. Retroviruses 0:0-0(1997).
BMBL, ARO11541; AAB65741.1; -.
InterPro; IRR00276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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Pan troglodytes (Chimpanzee).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Pan,
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MEDLINE-99335215; PubMed=10408730;
Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.C.,
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01-MAY-2000 (TEMBLrel. 13, Last sequence update)
01-JUN-2001 (TEMBLrel. 17, Last annotation update)
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                                                                                                                                                                                                                                                              Gorilla gorilla (gorilla).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalla: Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
NCBI_TaxID-9593;
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                                                                                                                                     AIDS Res. Hum. Retroviruses 15:479-483(1999).
EMBL, ARTOSZOI, AADZOSZOI, AADZOSZOI, PLEAPPO, PREMOMOZ76; GPCR.Rhodpsn.
PRAMNS: PRO0031; 7tm_1; 1.
PRINYS: PR00031; GPCRRHOODPSN.
PROSTIE; PS00237; GPROPEIN RECEP_FI_1; UNKNOWN_1.
PROSTIE; PS50262; G_PROTEIN_RECEP_FI_2; 1.
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Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
NCBL_TaxID=81572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Zhang Y., Ryder O.A., Zhang Y.;
"Sequence comparison of the CCR5 gene in primates and primate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phylogeny.";
Submitted (Aug-1999) to the EMBL/GenBank/DDBJ databases.
Bub. AF17/8999, AAR43382.1;
InterPro: IPR000276; GFCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                              Muchaer-Trutwin M.C., Corbet S., Hansen J., Diop O.,
Georges-Courbot M.-C., Barre-Sinoussi F., Fomsgaard A.;
Submitted (Nov-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF035214; AA044007.1; -
InterPro: IPR000276; GPCR_Rhodpsn.
Pfam; PF00011; 7tm.1; 1.
PROSTIE; PS00237; GPCRRHODOPSN.
PROSTIE; PS00237; GPRRHODOPSN.
PROSTIE; PS00237; GPRRHODOPSN.
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SEQUENCE 352 AA; 40481 MW; 2578AOF2C07A4A65 CRC64;
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Nasalis larvatus (Proboscis monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Shang Y.,
Sequence comparison of the CCR5 gene in primates and
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                                NCBI_TaxID-43780;
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Fubrited (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF177882; AAK43355.1; ...
InterPro; IPR000276; GPCR_Rhodpsn.
Pflam; PF00001; 7tm_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_FI_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_FI_2; 1.
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang Y., Ryder O.A., Zhang Y.;
"Sequence comparison of the CCR5 gene in primates and primate phylogeny.";
"Submitted (AUG-1999) to the EMBL/Genbank/DDBJ databases.
EMBL, AF177881; AAK43364.1;
InterPro: IPR000276; GPCR_Rhodpsn.
PROSITE; PS00037; G_PROTEIN_RECEP_F1.1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1.2; 1.
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Best Local Similarity:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spearman P.W., Mburu D.N., Graham B.S.;
Spearman P.W., Mburu D.N., Graham B.S.;
"Differential Utilization of CCR5 Molecules from Three East African Stains Species by the HIV-1 Envelope Glycoprotein.";
Submitted (APR-1999) to the EMBL/Genbank/DDBJ databases.
EMBL, AF141639, AAD32664.1;
-InterPro; IFP0000256, GPCR_Rhodpsn.
Pfam, PR00001; 7tm.1.1.
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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        Pygathrix avunculus (Tonkin snub-nosed monkey), and
Pygathrix roxellana (golden snub-nosed monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                                                                         primates.";
                                                                                                                         Zhang Y.-W., Zhang Y.-P.;

"Sequence evolution of chemokine receptor CCR5 gene in prim
"Sequence evolution of chemokine receptor CCR5 gene in prim
Submitted (JUN1998) to the EMEL/GenBank/DDBJ databases.
EMEL, AF075447; AAD19859.1;

EMBL, AF075447; AAD19856.1;

InterPro; IPR000276; GPCR_Rhodpsn.
PFANNYS; PR00127; Tem_1; 1.
PRINNYS; PR00127; GPRPATEIN RECEP_F11; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F12; 1.
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Matches:
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Mismatches:
Indels:
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                                                                                                             SEQUENCE FROM N.A.
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                                            Theropitheous gelada (Gelada baboon),
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Theropithecus.
                                                                                                                                        primate
                                                                                                                                                          to the EMBL/GenBank/DDBJ databases
                                                                                                      [1]
SEQUENCE FROM N.A.
Zhang Y., Ryder O.A., Zhang Y.;
"Sequence comparison of the CCR5 gene in primates and
                                                                                                                                                                                                                                  4D3643B6C13E90D5 CRC64;
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Pfan; PP00001; 7tm.1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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  Created)
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1716.50
95.75%
94.05%
65.32%
DEC-2001 (TIEMBLIEL 19, DEC-2001 (TIEMBLIEL 19, MAR-2002 (TIEMBLIEL 20, chemokine receptor 5.
                                                                                                                                                               EMBL; AF177891; AAK43374
InterPro; IPR000276; GPC
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Submitted (AUG-1999)
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           CAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG
                      CIGAAGAGCAIGACTGACAICTACCTGCTCAACCTGGCCAICTCTGACCTGITTTTCCTT
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                                                        TTCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGG
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Colobinae;

Trachypithecus;
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Last annotation update)
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PROSITE; PSO1237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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HisPheProTyrSerGlnTyrGlnPheTrpLysAsnPheGlnThrLeu-LysIleValIl
                                          CTTGGGGCTGGTCCTGCCTGCTTGTCATGGTCATCTGCTACTCGGGAATCCTAAAAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCRS.
Papio anubis (Olive baboon).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.
NCBI_TAXID=9555;
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1: 1.
PROSTITS; PR00237; GPCRHODOPSN.
PROSTITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; U.
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EMBL; AF141640; AAD32685.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Miopithecus.
NCBL_TaxID-36231;
                                                                                                                                                                                                                                                                                                     primate
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_l; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Matches:
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Zhang Y., Ryder O.A., Zhang Y.;

*Sequence comparison of the CCR5 gene
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01-DEC-2001 (TrEMBLrel. 19
01-MAR-2002 (TrEMBLrel. 20
C-C chemokine receptor 5.
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                                             ITCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGG 419
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ATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                       "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism."; AIDS Res. Hum. Retroviruses 0:0-0(1997). EMBL, AR011538; AR055738.1; -. Interpro; IPRO00276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                          Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G.,
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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352 AA; 40523 MW;
                                                                                                                   troglodytes (Chimpanzee).
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                                                                                  CCR5 receptor (Fragment).
PRELIMINARY;
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SEQUENCE FROM N.A.
STRAIN=MACCR5-140A;
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1 LeuProGlyIleIlePheThrArgSerGlnArgGluGlyLeuHisTyrThrCysSerSer 180	0 CATITICCAIAC	HisPheProTyrSerGlnTyrGlnPheTrpLysAsnPheGlnThr		0 eLeuGlyleuValLeuProleuLeuValMetValIleCysTyrSerGlylleLeuLysTh 220		0 rLeureuargCysArgAsnGluLysLysArgHisArgAlavalArgLeullePheThrIl 240		.0 eMetlleYalTyrPheLeuPheTrpAlaProTyrAsnIleValLeuLeuLeuAsnThrPh 260	7 CCAGGAATTCTTTGGCCTGAATAATTGCAGTAGCTCTAACAGGTTGGACCAAGCTATGCA 1046	-		0 ovalthrGluthrLeuGlyMetThrHisCysCysIleAsnProlleIleTyrAlaPheVa 300		0 lGlygluLysPheArgAsnTyrLeuLeuValPhePheGlnLysHisIleAlaLysArgPh 320		0 eCysLysCysCysSerIlePheGlnGlnGluAlaProGluArgAlaSerSerValTyrTh 340	_	0 rArgSerThrGlyGluGluGleSerValGlyLeu 352	
161	780	181	807	200	867	220	927	240	987	260	1047	280	1107	300	1167	320	1227	340	
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Search completed: June 3, 2003, 18:49:48 Job time: 119.268 secs

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June 3, 2003, 18:39:24; Search time 4.86523 Seconds (without alignments) 5149.005 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                              OM nucleic - protein search, using frame_plus_n2p model
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Xgapop 10.0 , Xgapext 0
Ygapop 10.0 , Ygapext 0
Rgapop 6.0 , Fgapext 7
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Database :	A Ge	A_Geneseq_101002:*
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	;	/SIDS2/gcgdata/geneseg/genesegp-emb1/AA1981.DAT:*
		/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
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	 	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
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	.; &	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
	6	/SIDS2/gcgdata/geneseq/genesegp-embl/AA1988.DAT:*
	10:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
	11	/SIDS2/gcgdata/geneseg/genesegp-embl/AA1990.DAT:*
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	17:	/SIDS2/gcgdata/geneseg/genesegp-emb1/AA1996.DAT:*
	18:	/SIDS2/gcgdata/geneseg/genesegp-embl/AA1997.DAT:*
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	22:	/SIDS2/gcgdata/geneseg/genesegp-embl/AA2001.DAT:*
	23:	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Description	AAW22408 Inactive human CCR AAW8823B HIV-1 co-receptor AAW37123 Human Chemokine re AAW37123 Human CCR5. How AAW37123 Human CCR5. How AAW37123 Human CCR5. How AAW3012B Human CCC chemokine re AAW3012B Human CCC chemokine re HUMA1012B Human CCR5 protein ch AAB8234B Human G-protein ch AAB07037 Human G-protein ch AAB07039 Human G-protein ch AAB07039 Human G-protein ch AAB07030 Human G-protein ch AAB07031 Human CCR5 protein ch AAB07034 Human CCR5 protein ch AAB07035 Human CCR5 protein ch AAB07036 Human CCR5 protein ch AAB07037 Human CCR5 protein ch AAB07038 Human CCR5 protein ch AAU70715 Human CCR5 protein ch AAW32824 Human CCR5 protein ch AAW32824 Human CCR5 protein ch AAW32833 Human CCR5 protein ch AAW32824 Human CCR5 protein ch	ALIGNMENTS 5 AA. the receptor 5; CCR5; type 1; type 2; HIV-1; HIV-2; agnosis; treatment; prevention; id arthritis; glomerulonephritis; iibrosis; psoriasis; viral infection; mmune disorder.
Length DB	200 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	d; Protein; 215 AA. rst entry) RS. Yys-Cys chemokine 1 ilency virus; type resistance; diagnos asas; rheumatoid an asas; rheumatoid an ic pulmonary fibros lerosis; autoimmuno
& Query Match	0000 922.7.7.9 922.7.7.9 922.7.7.7.9 922.7.7.7.9 922.7.7.7.9 922.7.7.7.9 922.7.9 922.7 922.7 922.7 922.7 922.7 922.7 922.7 922.7 922.7 922.7 922.7	08 standard; 108; -1998 (first ve human CCR5 ve; human CR5 position; resimmunodeficien position; resimmunodeficien; atheroscleriapiens.
Score	1009	274 274 APR APR cti cti lam hma cer
Result No.	11111111111111111111111111111111111111	RESULT 1 AAN27408 ID AAN27 XX AC AAN27 XX XX XX DE Inac' XX

103..124 /note= "transmembrane domain 3" 142..167 /note= "transmembrane domain 4"

98WO-EP03437. 97US-0048057.

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W09854317-A1
                                                                                          29-MAY-1998;
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                                                                       03-DEC-1998,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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     Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTC
                                                                                                                                                                                                                 The present sequence is an inactive human CC (cys-cys) chemokine receptor 5 (CYES), which lacks the last 3 transmembrane regions and the regions involved in G protein-coupling. CCK5 or its CDNA can used to diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis, viral infections, especially human manunodeficiency virus type 1 or type 2 (HIV-1 or HIV-2) infection, cancer, atherosclerosis and autoimmune disorders. Subjects that express the inactive receptor have a predisposition, or resistance to HIV-1 and/or HIV-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIV-1; CCR5; CCR5-delta32; co-receptor; infection; diagnosis; AIDS;
                                                                                                                                                       Active and inactive forms of human CC chemokine receptor CCR-5 useful to diagnose, prevent and/or treat inflammatory disorders,
                                                                                                                                                                                                                                                                                                                                                         215
31
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Matches:
Conservative:
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Indels:
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/note= "transmembrane domain 1" 67..87
                                                                                                            Samson M, Vassart G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "transmembrane domain 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 GlyAsnProLysAsnSerAlaSerValSerLys 215
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                                                                                                                                                                              autolmmune disease and viral infection
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                                                                                                                                                                                               Claim 7; Fig 1d-e; 94pp; English.
                                       97WO-BE00023
                                                         96EP-0870102
96EP-0870021
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100.00%
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                                                                                                           Parmentier M,
                                                                                       (EURO-) EUROSCREEN SA.
                                                                                                                            WPI; 1997-479829/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy; human.
                                                                                                                                                                                                                                                                                                                            215 AA;
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Best Local Similarity:
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WO9732019-A2
                                                         06-AUG-1996;
01-MAR-1996;
                                      28-FEB-1997;
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                   04-SEP-1997
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1 ATTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTC 60
                                                                                                                                                                                                                                                                                                                                                              designated CCR5-Gelta32. That includes the first 4 transmembrane domains of vild-type CCR5 (see AAW88232), but lacks transmembrane domains of vild-type CCR5 (see AAW88232), but lacks transmembrane domains of CCR5 serves as a co-receptor for infection by macrophage-tropic M-tropic) strains of HTV-1. Individuals homozygous for the CCR5-delta32 mutation are resistant to HIV-1 infection, but heterozygous individuals are susceptible. The invention additionally relates to the identification of variant CCR5. The detection of CCR5 transmembrane domains 3-7 of individuals at lower risk of infection relative to the general population who, if infected, may exhibit slower progression to diagnostic methods for detecting the presence of such variants. A LDS. Probes and primers (see AAV84127-36) are provided for use in diagnostic methods for detecting the presence of such variants. A method is provided for inhibiting HTV-1 infection of a cell capted conding a CCR5 receptor. This involves introducing a nucleic acid encoding a CCR5 variant into the cell, thereby reducing the number of functional CCR5 molecules present on the cell surface.
                                                                                                                                                                                                 New CCR5 variant protein of the HIV-1 co-receptor - useful in developing resistance of CCR5-expressing cells to HIV-1 infection
                                                                                                                                                                                                                                                                                                                                            This is the amino acid sequence of a CCR5 variant protein,
                                                            Braun J, Quillent C;
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Matches:
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                                                            Beretta A,
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                                                         Arenzana Siesdedos F,
                                                                                                            WPI; 1999-059835/05.
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Best Local Similarity:
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176 LeuLysileValileLeuGlyLeuValLeuProLeuLeuValMetValileCysTyrSer 195

AAW27407 standard; Protein; 352 AA.

RESULT

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GGAATCCTAAAAACTCTGCTTCGGTGTCGAAAT

62 961 human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention; inflammatory disease; Theumatory disease; Theumatory alonerulonephritis; glomerulonephritis; asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer; atherosclerosis; autoimmune disorder.

Homo sapiens WO9732019-A2.

Human Cys-Cys chemokine receptor 5; CCR5;

(first entry)

14-APR-1998

AAW27407;

Human CCR5,

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This protein comprises human MMIR-CCR, a novel C-C chemokine receptor associated with monocyte/macrophage infiltration and chemotaxis and haematopolesis. The amino acid sequence was deduced chemotaxis and haematopolesis. The amino acid sequence was deduced from a cDNA clone (see AAT9542) obtained from a cDNA library made from a cDNA clone (see AAT9542) obtained from a cDNA library made culture, i.e. cells associated with inflammation and culture, i.e. cells associated with inflammation and clumnomodulation. Another novel chemokine receptor, MPRG-CCR (see AAM36767), is also claimed. MMIR-CCR contains 7 transmembrane spanning sequents connected by a serives of infracellular and extracellular loops. MMIR-CCR and MPRG-CCR can be used to study, diagnose and treat disease states in which normal leukocyte cunction is perturbed by normal leukopolesis or inappropriate action activation via chemokine agonists or antagonists, such as infection, inflammation, proliferation, solid tumours, cardiovascular disease, abnormal cell proliferation, solid tumours, cardiovascular granulomatous disease, athma, myasthenia gravis, diabetes, choaise rusinaent such control of anthartis, alveolitis, atherosclerosis, chronic chadiar-usinaent such control of such control of such control of such control of chadiar-usinaent control of such control of chadiar-usinaent control of chadi
                 Mammalian mixed lymphocyte receptor; chemokine receptor; MMLR-CCR; human; monocyte; macrophage; chemotaxis; haematopoissis; infection; inflammation; proliferative disease; cardiovascular disease; tumour; rheumatoid arthritis; alveolitis; atherosclerosis; chronic granulomatous disease; asthma; myasthenia gravis; diabetes; inflammatory bowel disease; toxic shock syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotide encoding MMLR-CCR or MPHG-CCR chemokine receptor - useful to study, diagnose and treat, e.g. infection, inflammation, solid tumour and proliferative and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                /note= "a claimed polypeptide has isoleucine at residue 121"
                                                                                                                                                                                       septic shock; Chediak-Higashi syndrome; therapy; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coleman R, Wilde CG;
                                                                                                                                                                                                                                                                                                                                 107..128
/note= "conserved peptide"
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-US06993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1997-549729/50.
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                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-NOV-1997.
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                                                                                                                                                                                                                                                                                                                              Peptide
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The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5), which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3, interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha) chemokines. Active CCR-5 is also a receptor of human immunodeficiency virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can used to diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis, glomerulonephitis, asthma, idiopathic pulmonary fibrosis and psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer, atherosclerosis and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352
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152.00
100.00%
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92.68%
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Active and inactive forms of human CC chemokine receptor CCR-5 useful to diagnose, prevent and/or treat inflammatory disorders, autoimmune disease and viral infection

Samson M, Vassart G;

Libert F, Parmentier M, (EURO-) EUROSCREEN SA.

WPI; 1997-479829/44.

N-PSDB; AAT90117

97WO-BE00023.

28-FEB-1997; 06-AUG-1996;

04-SEP-1997,

96EP-0870021. 96EP-0870102.

01-MAR-1996;

2 TTAAAGATAGTCATCTTGGGGCTGGTCCTGCCTGCTTGTCATGGTCATCTGCTACTCG 61 US-09-938-703-3_COPY_792_885 (1-94) x AAW27407 (1-352)

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332 31 0 0 0

Conservative:

Matches: Length:

4.4e-13 152.00 100.00% 100.00%

Similarity:

Query Match:

Percent Similarity:

Alignment Scores:

Mismatches: Indels:

US-09-938-703-3_COPY_792_885 (1-94) x AAW26766 (1-332)

92.68% 18

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352 AA;
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196 LeuLysIleValIleLeuGlyLeuValLeuProLeuLeuValMetValIleCysTyrSer 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This polypeptide sequence comprises novel human chemokine receptor 88C, a G protein coupled receptor that is involved in leukocyte trafficking. Its amino sequence was deduced from a cobna cone (AA785161) isolated from a macrophage library. It shows 62% identity to CCCKR1. Chemokine receptor 88-2B (see AAW27124) has also been identified. 88C and 88-2B receptors and their polypeptide fragments can be produced in transformed host cells. The receptors, peptides comprising one or more of the extracellular or intranclular domains, and anti-receptor antibodies can be used to modulate receptor activities, particularly ligand and G protein binding, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding chemokine receptors 88-2B and 88C - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to modulate leukocyte trafficking, e.g. for treatment of
inflammation, tumours, viral infections, autoimmune diseases, etc.
                                                                                                                                                                                                                                     Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour; asthma; viral infection; ADS; inflammation; autoimmune disease; therapy; diagnosis; leukocyte trafficking; G protein coupled receptor; ligand; modulator; autibody; human.
                                             216 GlylleLeuLysThrLeuLeuArgCysArgAsn 226
                             62 GGAATCCTAAAAACTCTGCTTCGGTGTCGAAAT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                 /label- Extracellular_domain
125..145
/label- Intracellular_domain
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/label- Extracellular_domain
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/label= Intracellular_domain
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                                                                                                                                                                                                                                                                                                                                              Socation/Qualifiers
                                                                                                                  AAW27123 standard; Protein; 352 AA
                                                                                                                                                                                                        Human chemokine receptor 88C.
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213..235
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259..28
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2 TIAAAGATAGTCAICTIGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTCG 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human G-protein chemokine receptor, HDGNR10 - useful to identify (ant)agonists, for treatment of haematopoiesis, leukaemia, chronic and acute inflammation, rheumatoid arthritis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human mature G-protein chemokine receptor HDGNR10 (AAW07602)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G-protein chemokine receptor; HDGNRIO; signal transduction; haematopoiesis; leukaemia; inflammation; rheumatoid arthritis;
are potentially potentially useful in the treatment of atherosalerosis, rhemmatoid arthritis, tumours, asthma, viral infection, AlbS, inflammatory conditions, pathological immune response, abnormal haematopoletic processes etc.
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Mismatches:
Indels:
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Matches:
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N-PSDB; AAT44042.
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                                                                                                                                        352 AA;
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Best Local Similarity:
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WPI; 1998-032650/03.
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Best Local Similarity:
Query Match:
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                               N-PSDB; AAT76920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC chemokine receptor 5; CCR5; G-protein coupled receptor; human immunodeficiency virus; HIV; CD4; AIDS; therapy;
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Feng Y, Kennedy PE, Murphy PM;
                                                                                                                                           US-09-938-703-3_COPY_792_885 (1-94) x AAW07602 (1-352)
                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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/note= "transmembrane domain"
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/note= "transmembrane domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Human CC chemokine receptor 5 (CCR5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
29..55
/label- I
                                                                                                                                                                                                                                                                                                                                               AAW23835 standard; Protein; 352 AA.
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/label= III
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/note= "ex
277..300
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194..219
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                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transgenic animal.
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            Alignment Scores:
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Query Match:
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Domain
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                            Pred. No.:
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This protein sequence comprises of a novel human macrophage-selective CC chemokine receptor that has been designated CCR5. The sequence was deduced from an isolated obox clone (see AAT/6920). An Ala12/Leu variant (see W28840 of CCR5 was also identified. The susceptibility of human macrophages to HIV infection depends on cell surface expression of CD4 and CCR5. CCR5 is a member of the 7-transmembrane superfamily of G-protein coupled cell surface molecules. It plays an essential role in the membrane fusion step of infection by some HIV isolates. The establishment of stable, non-human cell lines and transgenic mammals having cells that coexpress human CD4 and CCR5 provides valuable tools for research of HIV infection.

Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding agents capable of blocking membrane fusion between HIV and target cells represent potential anti-HIV therapeutics for macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS; gene therapy; human.
  - used to inhibit membrane
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Conservative:
Mismatches:
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142..167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
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CC chemokine receptor 5 polypeptide fusion between HIV and a target cell
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32..56
/note= "transmembran
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                                                                               Claim 68; Fig 1C; 70pp; English.
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200..223
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This is the amino acid sequence of wild-type human CCRS, which serves as a correceptor for infection by macrophage-tropic (M-tropic) strains of HIV-1. The invention relates to the dentification of a CCRS variant (see AAW80231), designated CCR5m303, comprising the first two transmembrane domains of wild-type CCR5, but lacking transmembrane domains 3-7. The presence of the CCR5m303 variant with the wild type CCR5 allele shows a positive correlation with resistance to infection with M-tropic HIV-1 strains, and may indicate slower progression of the disease. The detection of CCR5 variants may be used to identify individuals at lower risk of infection relative to the general population who, if infected, may exhibit slower progression to AIDS. Probes and for detecting the presence of such variants. A method is provided for inhibiting HIV-1 infection of a cell expressing the CCR5 or inhibiting HIV-1 infection of a cell expressing the CCR5 variant into the cell, thereby reducing the number of functional cCR5 molecules present on the cell surface.
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                                                                                                                                                                                                                                                                                                              New CCR5 variant protein of the HIV-1 co-receptor - useful in developing resistance of CCR5-expressing cells to HIV-1 infection
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           236..260
/note= "transmembrane domain 6"
275..301
/note= "transmembrane domain 7"
 domain 5"
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/note- "transmembrane
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N-PSDB; AAV84126.
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              Domain
                                            Domain
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The present sequence represents a human G-protein chemokine receptor designated HDGNR10. HDGNR10 polynucleotides are useful in methods of screening for compounds which bind to and either: (1) activate the HDGNR10 polypeptides causing stimulation of haematopolesis, wound healing, coagulation, and anglogenesis; treatment of solid tumours, chronic infections, leukaemia, T-cell mediated autoimmune diseases, parasitic infections, psoriasis, and to stimulate growth factor activity; or (2) inhibit activation of the HDGNR10 polypeptides which as beful for preventing and/or treating allery, atherogenesis anaphylaxis, malignancy, chronic and caute inflammation, histamine and immunoglobulin E-mediated alleryic reactions, prostaglandin-independent arbitis shock and hyper-eosinophilia syndrome. The polymucleotides are also useful for diagnostic assays for detecting diseases related to mutations in the nucleic caid sequences encoding the polymetides and for detecting an altered level of the soluble form of the receptor collypeptides. The purposes of the soluble form of the receptor of the substitute of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ITAAAAGATAGICAICITGGGGCIGGICCIGCCGCIGCIIGICAIGGICAICIGCIACICG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid encoding human G-protein chemokine receptor useful for diagnostic assays, scientific research and screening for compounds which bind to and activate or inhibit activation of the
                                          Human; G-protein coupled receptor; G-protein chemokine receptor;
HDGNR10; diagnosis; haematopoiesis; wound healing; coagulation;
                                                                                          angiogenesis; tumour; infection; leukaemia; psoriasis; allergy; real mediated autoimmune disease; atherogenesis; anaphylaxis; inflammation; allergic reaction; silicosis; sarcoidosis; rheumatoid arthritis; hyper-eosinophilia syndrome.
Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                            95US-0466343.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAZ91481.
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                                                                                                                                                                                                                                                                                                                                                            06-JUN-1995;
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Human CCR5 protein.
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                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                         The invention relates to G protein-coupled receptors (GPCRs) for which the endogenous ligand has been identified. Non-endogenous constitutively activated versions of known GPCRs are used in the invention for the direct identification of candidate compounds as
                                                                                                                                                                                                                                                                                                     use in
                                                                                                                                                                                                                                                                                                                                                                                               receptor agonists, inverse agonists or partial agonists. Such agonists are useful as therapeutic agents for diseases or disorders associated with GPCRs. The present sequence is a non-endogenous version of a known human GPCR.
                                                                                                                                                                                                                                                                                            Identifying agonists of G protein-coupled receptors (GPCRs) for a disease treatment, comprises contacting candidate compounds with versions of GPCRs.
                                                                                              GPCR; non-endogenous; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-938-703-3_COPY_792_885 (1-94) x ABB56342 (1-352)
                                                                           Non-endogenous human GPCR protein, SEQ ID NO: 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches:
Conservative:
Mismatches:
Indels:
                                                                                            Human; G protein-coupled receptor; GPCR; non-end
constitutively activated GPCR; agonist; disease.
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                 ABB56342 standard; Protein; 352
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                                                       (first entry)
                                                                                                                                                                                                                                  (AREN-) ARENA PHARM INC.
                                                                                                                                                                                                                                                    Lehmann-Bruinsma K,
                                                                                                                                                                                                                                                                      WPI; 2001-648759/74
                                                                                                                                                                                                                                                                                                                                                                                                                                              352 AA;
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                                                                                                                                                                                                                                                                                 N-PSDB; ABI97978
                                                                                                                                                     WO200177172-A2.
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                                                                                                                          Homo sapiens.
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                                                       18-FEB-2002
                                                                                                                                                                        18-OCT-2001
                                                                                                                                    Synthetic.
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                                    ABB56342;
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RESULT 10
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This invention describes a novel diagnostic agent (A) comprising at least two different ligands (I) for receptors (II) that are implicated in disease. (A) are used for the diagnosis of tumors (especially colorectal or prostatio), organ rejection, inflammation and autoimmune diseases.

Also inhibitors of (I) are used therapeutically against tumors (and their metastases), inflammation (particularly bronchial asthma or chronic bowel inflammation), or autoimmune diseases (rhemmatiod arthritis or lupus), where the (cardo)vascular, lymphatic, respiratory, nervous, digestive, endocrine, motor or urogenital systems or skin are affected, and bone marrow diseases. The products of the invention are chemokine derivatives which have cytostatic, antiinflammatory, antiasthmatic, immunosuppressive, dermatological, antiinheumatic, antiarthritic.

Chemokines act on specific tumor and inflammatory cells through a constellation of chemokine receptors (CR), which control migration and proliferation of these cells. Ad80045-Ad80128 represent human chemokine fragments used to illustrate the method of the invention.
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Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection; inflammation; autoimmune disease; metastasis; bronchial asthma; lupus; chronic bowel inflammation; rheumatiod arthritis; cytostatic; antiinflammatory; antiathmatic; immunosuppressive; dermatological; antirheumatic; antiarthritic.
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                       02-APR-2001; 2001WO-EP03708.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-626256/72.
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AAB82948;

07-SEP-2001

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The specification describes an antibody which is specific for an antigenic fragment of gpl20. This antigenic fragment binds to DC-SIGN or is exposed upon gpl20 binding of DC-SIGN due to concomitant conformational change. DC-SIGN is a receptor that is specifically expressed on dendrific cells and facilitates infection of T lymphocytes with HIV. DC-SIGN is identical to a HIV-1 gpl20-binding C-type lectin. DC-SIGN binds is identical to a HIV-1 gpl20-binding C-type lectin. DC-SIGN binds is identical to a HIV-1 gpl20-binding C-type lectin. DC-SIGN binds attainty. The antibody of the invention inhibits the trans can antibody is useful to treat or prevent HIV infection. The present sequence represents a human CCR5 protein, which is a translocation promoting agent that interacts with CD4.

This receptor functions in HIV-1 entry into cells.
196 LeuLysIleValIleLeuGlyLeuValLeuProLeuLeuValMetValIleCysTyrSer 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          An antibody for the treatment or prevention of HIV-infection comprises a gpl20 portion which binds to DC-SIGN or is exposed upon gpl20 binding of DC-SIGN due to concomitant conformational change -
                                                                                                                                                                                                                                                                                                                                                     Human; receptor; DC-SIGN; dendritic cell; I lymphocyte; HIV; gpl20; C-type lectin; ICAM3; HIV entry; I cell; macrophage; HIV infection; CCR5.
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Matches:
Conservative:
                                                                        216 GlylleLeuLysThrLeuLeuArgCysArgAsn 226
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                                              62 GGAATCCTAAAACTCTGCTTCGGTGTCGAAAT
                                                                                                                                                                                                                                                                                                                Amino acid sequence of human CCR5 protein.
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                                                                                                                                                                              AAG79089 standard; Protein; 352 AA.
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Query Match:
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                                                                                                                                      RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel compounds comprising specific amino acids within CCR5 (HIV 1 co-receptor) amino terminal domain including negatively charged and two sulfated tyrosine residues is useful for treating HIV infection in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of human HIV-1 co-receptor CCR5.

Amino acids 2-18 in the N-terminal region of CCR5 comprise an HIV-1 sp120-binding site that determines the specificity of the interaction between CCR5 and HIV-1 sp120. Post-translational sulfation of the tyrosine residues in the CCR5 N-terminus is required for sp120 binding and may critically modulate the susceptibility of target cells to HIV-1 infection in vivo. The invention provides claimed sulfated peptides (see AABB294) that are based on the CCR5 N-terminal region and which are effective for inhibiting HIV-1 binding to CCR5. These peptides are used in claimed methods of inhibiting HIV infection of CH4+ cells, of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preventing CD4+ cells from becoming infected with HIV, of treating a subject whose CD4+ cells are infected with HIV, of treating identifying an agent which inhibits binding of a CCR5 ligand to a CCR5 receptor. The methods may be carried out in a subject, especially a human, infected (therapeutic method), not infected with HIV (prophylactic method), or in a subject who is not infected with, but has been exposed to, HIV.
                                                                                                                               CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1; infection; therapy; vaccine; anti-HIV-1.
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Matches:
Conservative:
Mismatches:
Indels:
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/note= "binds to HIV-1 gp120"
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                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                   Human HIV-1 co-receptor CCR5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-FEB-2000; 2000US-185667P.
                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2001; 2001WO-US06699.
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N-PSDB; AAH26903.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                              WO200164710-A2.
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2 TIAAAGAIAGICAICITGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTCG 61
US-09-938-703-3_COPY_792_885 (1-94) x AAG79089 (1-352)
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2 TTAAAGATAGTCATCTTGGGGCTGGTGCTGCTGTTGTCATGGTCATCTGCTACTCG 61

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Sequence

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Best Local S: Query Match:

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protein. CRS Hooker as immand of the care control (CACA) incorrect protein. CRS Hooker as a notated with inflammation, defective or aberrant chemotaxis of immune cells, HIV infection (such as Preumocystis carfull chemotaxis of immune cells, HIV infection (such as Preumocystis carfull presenting cell interaction. The disease or disorder may also be an infectious disease (e.g. a viral infection such as mearly stage HIV infection, a cytomegalovirus infection, or a poxyirus infection), an infection, a cytomegalovirus infection, or a poxyirus infection), an infection, a cytomegalovirus infection, or a poxyirus infection), an infection, a cytomegalovirus infection, or a poxyirus infection), an infection, a cytomegalovirus infection, or a poxyirus infection), an infection, a cytomegalovirus infection, or a poxyirus infection), an infection, a cytomegalovirus infection, or a poxyirus infection), and infection, action infection, architis) or a neurodegenerative carcassion, lack of CCRS function, aberrant CCRS ligand expression, or consistent in such disand function. CCRS HORNIO protein is used as a food additive or preservative to increase or decrease storage capabilities. CCRS HORNIO DNA are useful for chromosome identification and in gene crassic ovary, adrenal gland, bone, bone marrow, gastrointestinal tract, breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, colliss, cardiovascular disorders (myocardial ischaemias) and ulcerative colliss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence is human G-protein chemokine receptor (CCR5) HDGNR10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
                                                                                                                                                                       Isolated nucleic acid encoding a human G-protein chemokine receptor (CCR5) HDSMR10 Polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
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Mismatches:
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                                                                                             Li Y, Ruben SM;
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                                                                                                                                                                                                                                                      Claim 102; Fig 1; 495pp; English.
09-FEB-2000; 2000US-0181258,
09-MAR-2000; 2000US-0187999.
22-SEP-2000; 2000US-0234336.
                                                                SCI INC
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                                                                                             Roschke V,
                                                              (HUMA-) HUMAN GENOME
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Best Local Similarity:
                                                                                                                                             N-PSDB; AAD13181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    wound healing.
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                                                                                                                                                                                                                                 human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive; noctropic; neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; mandiple sclerosis; ulcerative colitis; Crohn's disease; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.
                                                                                                                                                                                                                       Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
                                                                                                                                                                                        Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.
                  216 GlylleLeuLysThrLeuLeuArgCysArgAsn 226
62 GGAATCCTAAAACTCTGCTTCGGTGTCGAAAT 94
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/label= Transmembrane_domain
/note= "Segment 3"
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|abel= Transmembrane_domain
|note= "Segment 4"
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note= "Segment 5"
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/label= Transmembrane_domain
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/label= Intracellular_loop_1
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/label= Transmembrane_domain
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|abel= Extracellular_loop_1
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                                                                                          AAE07037 standard; Protein; 352 AA.
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306..352
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label= E
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Domain
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immunodeficiency virus; antimicrobial; vasodilator; vulnerary;

cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy, neurodegenerative disorder; Raposi's sarcoma; autoimmune disease; rheumatcid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; hemolytic anemnia autoimmune thyroiditis, diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.

Homo sapiens.

WO200158915-A2

16-AUG-2001

09-FEB-2001; 2001WO-US04152.

09-FEB-2000; 2000US-0181258. 09-MAR-2000; 2000US-0187999. 22-SEP-2000; 2000US-0234336.

(HUMA-) HUMAN GENOME SCI INC

Li Y, Ruben SM; Rosen CA, Roschke V,

WPI; 2001-488965/53.

N-PSDB; AAD13198

Isolated nucleic acid encoding a human G-protein chemokine receptor (CCR5) BOSMR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.

Example 40; Page 486-487; 495pp; English.

The present sequence is human G-protein chemokine receptor (CCR5) HDGNRIO protein. CCR5 HGGNRIO antibodies are useful for treating, preventing or ameliorating a disease or disorder associated with inflammation, defective or aberrant chemotasis of immune cells, HTV infection (such as person T-cell antigen presenting cell interaction. The disease or aberrant T-cell antigen presenting cell interaction. The disease or disorder may also be an infection disease (e.g. a viral infection such as an early stage HTV infection, a cytomegalovirus infection, or a cytomegalovirus infection, or a neurodegenerative disorder. The disease or disorder may be associated or neurodegenerative disorder. The disease or disorder may be associated or uth aberrant CCR5 expression, lack of CCR5 function. Determat CCR5 in a neurodegenerative disorder. The disease or disorder may be associated or is used as a food additive or preservative to increase or decrease control of some capabilities. CCR5 HGCNRIO DNA are useful for chromosome identification and in gene therapy. CCR5 HGGNRIO DNA, protein, cantibodies, agonists and antagonists are also useful in the disposal procession of cancer (breast, overly, adrenal breast, broas procession) and prevention of cancer (breast, overly, adrenal breast broast procession).

Sequence 352 AA;

wound healing

gland, bone, bone marrow, gastrointestinal tract, liver, lug, urogenital); immune disorders (Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple solerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular disorders (myocardial ischaemias) and

352 31 0 0 0 Conservative: Mismatches: Matches: Indels: Length: 152.00 100.00% 100.00% 92.68% 4.4e-13 Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: Pred.

2 TTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGCTCTCTGCTACTCG 61

US-09-938-703-3_COPY_792_885 (1-94) x AAE07039 (1-352)

196 LeuLysIleVallleLeuGlyLeuValLeuProLeuLeuValMetValIleCysTyrSer 215 셤

62 GGAATCCTAAAAACTCTGCTTCGGTGTCGAAAT 94

ă 셤 Search completed: June 3, 2003, 18:45:06 Job time: 5.86523 secs

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21, Appl
4, Appli
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Fatent No. 6448375
GENERAL INFORMATION.
GENERAL INFORMATION.
APPLICANT: SAMSON, MICHEL
APPLICANT: PARKENTIER, MARC
APPLICANT: PARKENTIER, MARC
APPLICANT: LIBERT
APPLICANT: LIBERT
APPLICANT: LIBERT
APPLICANT: AND UCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROODDE, MARTENS, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 53,
Sequence 53,
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Sequence 55,
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Sequence 5
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Sequence 9
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Sequence 4
Sequence 1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
US-08-466-343D-9
US-08-466-343D-9
US-08-446-693-4
US-09-045-583-50
US-09-045-583-50
US-09-045-583-50
US-09-534-185-51
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US-09-534-185-54
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US-09-534-185-55
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APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
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STATE: CA
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    COUNTRY: U. ZIP: 92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-833-752-13
    Command line parameters:
-WODEL-frame+.n2p.model-DEW-xlp
-WODEL-frame+.n2p.model-DEW-xlp
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-USP-GSR2_1/USPPO_SPOOl/USO9938703/runat_03062003_161408_22885/app_query.fasta_1.1870
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-USPR-USO9938703_6CN 1_1.42_frunat_03062003_161408_22885 -NCPL-6 -ICPU-3
-NO_WMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
-DSY_TIMEOUT-120 -WARRN TIMEOUT-30 -THERBADS-1 -XGAPOP-10 -XGAPENT=0.5 -FGAPOP-6
-FGAPENT=7 -YGAPOP-10 -YGAPENT=0.5 -DELEXT=7
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Sequence 13, Appl
Sequence 14, Appl
Sequence 2, Appli
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52, Appl
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Sequence 6, Appli
Sequence 11, Appl
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3063.973 Million cell updates/sec
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                                                                                                                                                                                                                                                               1 ATTAAAGATAGTCATCTTGG..........CICTGCTTCGGTGTCGAAAT 94
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                                                                                                                                            June 3, 2003, 18:44:09 ; Search time 1.80534 Seconds
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUB_COMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                      using frame_plus_n2p model
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US-09-087-232A-17
US-08-833-752-6
US-08-833-752-11
US-08-466-343D-2
US-09-087-232A-13
US-08-861-105-14
US-08-575-967A-2
US-09-045-583-52
US-09-534-185-52
US-09-534-185-52
US-09-534-185-52
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                                                                                                                                                                                                                         US-09-938-703-3_COPY_792_885
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0, Xgapext (
Ygapop 10.0, Ygapext (
Fgapop 6.0, Fgapext (
Delop 6.0, Delext
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Maximum DB seq length: 200000000
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                                                                                                      protein search,
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1164
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Sequence 6, Application US/08833752
Patent No. 6448375
Patent No. 6448375
Patent No. 6448375

Patent No. 6448375

PAPLICANT: SAMSON, MICHEL
APPLICANT: BARNATION:
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: ACTIVE AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE:
STREET: 620 Newport Center Drive 16th Floor
CONTY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATTAMAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATGTCTGCTACTC 60
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US-09-938-703-3_COPY_792_885 (1-94) x US-09-087-232A-17 (1-215)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER REACABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                         205 GlyAsnProLysAsnSerAlaSerValSerLys 215
                                                                                                                 61 GGGAATCCTAAAAACTCTGCTTCGGTGTCGAAA 93
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FILING DATE: 9-APR-1997
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% Sequence 11, Application US/08833752

% Patent No. 6448375

% GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acid
TYPE: amino acid
TOPOLOGY: linear
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100.00%
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Best Local Similarity:
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Patent No. 6153431
APPLICANT: 0.151401
APPLICANT: 0.111lent et al.
TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                           1 ATTANAGATAGICATCITGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTC 60
                                                                                                                                                                                                                                                                                             4 IleLysAspSerHisLeuGlyAlaGlyProAlaAlaAlaCysHisGlyHisLeuLeuLeu 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIDM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBRE: US/09/087,232A
FILING DATE: 28 MAY 1998
CLASSIFICATION NUMBER: 60/048,057
FILING DATE: 30 MAY 1997
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 35,225
REGISTRATION NUMBER: 35,225
REGISTRATION NUMBER: 35,225
REGISTRATION NUMBER: 35,225
TELECHOMOTICATION INFORMATION:
TELECHOMOTICATION INFORMATION:
TELECHOMOTICATION INFORMATION:
TELECHOMOTICATION INFORMATION:
TELECHOMOTICATION INFORMATION:
TELECHOMOTICATION INFORMATION:
TELECHOMOTICATION OF SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
                                                                                                                                                                                                                                  US-09-938-703-3_COPY_792_885 (1-94) x US-08-833-752-13 (1-34)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole STREET: 30 Rockefeller Plaza
                                                                                                34
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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3GY: linear
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Best Local Similarity:
Query Match:
DB:
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STATE: New York
COUNTRY: USA
                                                                                                                                   Percent Similarity:
Best Local Similarity:
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10112
  STRANDEDNESS:
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Pred. No.:
                                                                              Alignment Scores:
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                  ; TOPOLOGY:
US-08-833-752-13
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Patentin Release #1.0, Version #1.30
                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,343D
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
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REGISTRATION NUMBER: 35,225
REFERENCE/DOCKET NUMBER: AP 31115
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,057
FILING DATE: 30 MAY 1997
ATTORNEY/AGERT INFORMATION:
                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, BRIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
IFLEFAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 408-2628
TELEFAX: (212) 765-2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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100.00%
100.00%
92.68%
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                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-466-343D-2
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: PARMENTIER, MARC
APPLICANT: UNSERT, GILBERT
APPLICANT: LIBERAT GILBERT
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESS:
ADDRESSE: G10 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATENTIN DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
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Mismatches:
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Matches:
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHRACTERISTICS:
LEBNGTH: 54 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
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100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                          U.S.A.
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Best Local Similarity:
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                                                                                                                                                                                                                                           92660
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Sequence 13, Application US/09087232A

Patent No. 6153431

GENERAL INFORMATION:

APPLICANT: Quillent et al.

APPLICANT: Quillent et al.

TITLE OF INVENTION: HUMAN IMMUNOBERICIENCY VIRUS CO-RECEPTOR

TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS: 2

ADDRESSER: Baker & Botts, L.L.P. attn. Lisa Kole

STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 TTAAAGATAGTCATCTTGGGGCTGGTCCTGCCTGCTTGTCATGGTCATCTGCTACTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-938-703-3_COPY_792_885 (1-94) x US-08-466-343D-2 (1-352)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/087,232A
FILING DATE: 28 MAY 1998
CLASSIFICATION: 435
1488.1150000/EKS/KLM
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216 61y11eLeuLysThrLeuLeuArgCysArgAsn 226
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2 TIAAAGAIAGICAICITGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTCG 61
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APPLICANT: Gray et al.

TITLE OF INVENTION: 0.6

NUMBER OF EXQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, 0.Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: 0.10cago

STATE: 111hois

COUNTRY: USE
                                                                                                                                                                                                                                                                                                                                                                   US-09-938-703-3_COPY_792_885 (1-94) x US-08-861-105-14 (1-352)
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OTHER INFORMATION: /= "88C amino acid sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
DERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                               Gaps:
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APPLICATION NUMBER: US/08/575,9672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6255184and, Greta E.
RESISPRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 35,302
RELECOMMUNICATION INFORMATION:
TELEPHONE: 206-485-1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-575-967A-2; Sequence 2, Application US/08575967A; Patent No. 6265184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 206-485-1662
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
                                                                                                                                                                                                                          3.52e-14
152.00
100.00%
100.00%
92.68%
  LENGIH: 352 amino acids IYPE: amino acid
                                                                                                                                           ORGANISM: Homo sapiens
                                        STRANDEDNESS: single
                                                                             MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                                                                                                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                   Percent Similarity:
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Pred. No.:
Score:
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                                                                TOPOLOGY:
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APPLICANT: DENG, HONGKUI
APPLICANT: DENG, HONGKUI
APPLICANT: DENG, HONGKUI
APPLICANT: LANDAU, NATHANIEL R.
APPLICANT: LANDAU, NATHANIEL R.
APPLICANT: LANDAU, NATHANIEL R.
APPLICANT: LANDAU, NAGROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: WACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TORKESPONDENCES: 14
CORRESPONDENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                             US-09-938-703-3_COPY_792_885 (1-94) x US-09-087-232A-13 (1-352)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216. GlylleLeuLysThrLeuLeuArgCysArgAsn 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                62 GGAATCCTAAAAACTCTGCTTCGGTGTCGAAAT 94
                                                                                                                                                                               Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 1049-1-004 N1
TELECOMONICALION INFORMATION:
TELEBENOME: 201-487-580
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/666,020
FILING DATE: 19-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION: DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/227,319
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-861-105-14; Sequence 14, Application US/08861105; Patent No. 6258527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
13:
                                                                                                                                                                               3.52e-14
                                                                                                                                                                                                152.00
100.00%
100.00%
92.68%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
            SEQUENCE CHARACTERISTICS:
    LENGTH: 352 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
    MOLECULE TYPE: protein
US-09-087-232A-13
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Floor
CITY: Backensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                            Alignment Scores:
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APPLICANT: Kwon, Douglas S.
APPLICANT: Wook, Yestte
APPLICANT: Gailtenbeck, Theo
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
TITLE OF INVENTION: CELLS
FILE REPERBENCE: 1049-1-017
CURRENT APPLICATION NUMBER: US/09/517,605
CURRENT PILING DATE: 2000-03-02
SUMBER: PATENTING DATE: 2.0
SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-09-534-185-52
US-09-534-185-52
Sequence 52, Application US/09534185
Sequence 52, Application US/09534185
Fatent No. 6403767
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION:
Heptahelical Receptor Superfamily and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 TTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTCG
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COUNTRY: USA
ZIP: 02109
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
CONFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: CURNOWN>
PRIOR APPLICATION: ADAIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-938-703-3_COPY_792_885 (1-94) x US-09-517-605-5 (1-352)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 GlyIleLeuLysThrLeuLeuArgCysArgAsn 226
  62 GGAATCCTAAAAACTCTGCTTCGGTGTCGAAAT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESSE:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels:
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                                                                                                    Sequence 5, Application US/09517605; Patent No. 6391567; GENERAL INFORMATION: APPLICANT: Littman, Dan R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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100.00%
100.00%
92.68%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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                                                             RESULT 10
US-09-517-605-5
                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.:
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                                                                                                                                                                                                                                                                                                                          03-09-045-583-52
; Sequence 5.2. Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Grand, Gerard J. et al.
; TITLE OF INVENTION:
NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street.
                                                                                                                                          2 TIAAAGATAGTCATCTTGGGGCTGGTCCTGCCTGCTTGTCATGGTCATCTGCTACTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-938-703-3_COPY_792_885 (1-94) x US-09-045-583-52 (1-352)
                                                                                                    US-09-938-703-3_COPY_792_885 (1-94) x US-08-575-967A-2 (1-352)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPETWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
  Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                   62 GGAATCCTAAAAACTCTGCTTCGGTGTCGAAAT 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: MIL-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)72-4214
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Massachusetts
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Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
STATE: Massac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
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Alignment Scores:
Pred. No.:
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APPLICANT: SAMSON, MICHEL
APPLICANT: PARNEWTIER, MARC
APPLICANT: PARNEWTIER, MARC
APPLICANT: LIBERT, FREDERICK
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: ACTIVE AND WOLLEC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: ADDRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-938-703-3_COPY_792_885 (1-94) x US-09-534-185-52 (1-352)
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 GlylleLeulysThrLeuLeuArgCysArgAsn 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 GGAATCCTAAAACTCTGCTTCGGTGTCGAAAT 94
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUTICATION INFORMATION:
TELEPRONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHRACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                        TOPOLOGY: linear
NOLECULE TYPE: peptide
FRAGENT TYPE: Internal
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-534-185-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-833-752-5; Sequence 5, Application US/08833752; Patent No. 6448375; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                         3.52e-14
152.00
100.00%
100.00%
92.68%
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LENGTH: 352 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-833-752-5
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
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2 IIAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTCG 61
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                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: L1, Y1
TILLE OF INVENTION: CHEMOKINE RECEPTOR HDGNRIO (AS AMENDED)
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: L100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-938-703-3_COPY_792_885 (1-94) x US-08-466-343D-9 (1-344)
                                                                                                                                         US-09-938-703-3_COPY_792_885 (1-94) x US-08-833-752-5 (1-352)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUBBER: 36,688
REGISTRATION NUBBER: 36,688
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFONE: (202) 371-2600
TELEFAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,343D
FILING DATE: 06-UN11995
CLASSIFICATION: 435
                                       Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                              216 GlyIleLeuLysThrLeuLeuArgCysArgAsn 226
                                                                                                                                                                                                                                                           62 GGAATCCTAAAAACTCTGCTTCGGTGTCGAAAT 94
Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 9, Application US/08466343D
; Patent No. 6025154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.41e-11
134.00
100.00%
96.30%
81.71%
                    152.00
100.00%
100.00%
92.68%
  3.52e-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
HOLECULE TYPE: protein
US-08-466-343D-9
                             Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
UNGHER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto
CITY: Palo Alto
STATE: California
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100.00%
96.30%
81.71%
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MOLECULE TYPE: protein
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                         ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, ADDRESSEE: STUART & OLSTEIN STREET: 6 Becker Farm Road
                                                                                                                                                                                  APPLICANT: Soppet, Daniel R.
APPLICANT: Yi, Li
APPLICANT: Ruben, Steven M.
APPLICANT: Rosen, Craig A.
ITILE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,244
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Ferrarco, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32800-445
FELECOMMUNICATION INFORMATION:
TELEPRONE: 201-994-1700
TELEPRA: 201-994-1744
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
                US-08-450-393A-4
; Sequence 4, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 ACTCTGCTTCGGTGTCGAAAT 94
                                                                                                                                : Sequence 3, Application US/08461244
: Patent No. 5776729
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100.00%
96.30%
81.71%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                   CITY: Roseland
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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                                                                                                              US-08-461-244-3
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208 IleLeuGlyLeuValLeuProLeuLeulleMetVallleCysTyrSerGlylleLeuLys 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-938-703-3_COPY_792_885 (1-94) x US-08-450-393A-4 (1-360)
ZIP: 94306-2155

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATION: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Realease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CSERT, Luan
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/02US
TELECOMMUNICATION INFORMATION:
TELECHHONE: 415-885-1655
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Conservative:
Mismatches:
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Job time: 2.80534 secs
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                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-883, C.T. TELEFAX: 416-883, C.T. TELEX: 380816CooleyPA; INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHRRACTERISTICS: LENGTH: 360 amino acids TYPE: amino acids ''. A sar
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us-09-938-703-6.rai

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1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
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Matches 215; Conservative
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   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STAIE: New York
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10112
                                                                                                                                                                                                                                                                                                                                      RESULT 1
US-09-087-232A-17
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 Query Match
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Sequence 6, Appli
Sequence 4, Appli
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5, Appli
2, Appli
9, Appli
3, Appli
4, Appli
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50, Appl
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Sequence 14, Appl
Sequence 2, Appli
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Appli
                                                                                                                 (without alignments)
201.057 Million cell updates/sec
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                                                                                                                                                                         1122
1 MDYQVSSPIYDINYYTSEPC......AACHGHLLLGNFKNSASVSK 215
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                                                                                                 June 3, 2003, 19:21:31 ; Search time 31.4634 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-087-232A-17
US-08-833-752-6
US-08-833-752-6
US-09-087-232A-13
US-08-66-105-14
US-08-66-105-14
US-08-68-375-96-78
US-08-46-383-752-5
US-08-46-343D-5
US-08-46-343D-5
US-08-46-343D-5
US-08-46-343D-5
US-08-46-343D-9
US-08-46-343D-9
US-08-46-343D-9
US-08-46-343D-9
US-08-46-343D-9
US-08-46-343D-9
US-08-46-383A-4
US-08-46-383A-4
US-08-46-383A-4
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US-09-534-185-50
PCT-US95-00476-4
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US-08-012-988A-2
US-08-450-393A-5
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                                                                                                                                                                                                                                                             262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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                                                                                                                                                                                         Sequence:
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Perfect
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Gaps

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GENERAL INFORMATION:
APPLICANT: Quillent et al.
APPLICANT: Quillent et al.
TITLE OF INVENTION: HUMAN IMMUNOBERCIENCY VIRUS CO-RECEPTOR
TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKET & Botts, L.L.P. attn. Lisa Kole
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                      Sequence 1, Ap
Sequence 54, A
Sequence 54, A
                                                                                                                                                                                                                                                                                                                                                                         Sequence 54, P
Sequence 8, Approved 8, Approved 18, P
                                                                            Sequence 9, Al
Sequence 53, 1
Sequence 53, 1
Sequence 20, 1
                                                                                                                                                                                                   Sequence 55,
Sequence 55,
Sequence 15,
     Sequence 5
Sequence 1
Sequence 5
                                                                                                                                                                                                                                                                          Sequence A
                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/087,232A
FILING DATE: 28 MAY 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,057
FILING DATE: 30 MAY 1997
ATTORNEY AGENT INFORMATION:
NAME: KOLE, LISA B.
REGISTRATION NUMBER: 35,225
REFERENCE/POCKET NUMBER: 35,225
REFERENCE/COCKET NUMBER: AP 31115
TELEPHOME: (212) 765-2519
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: Amino acids
TYPE: Amino acids
US-08-446-669-5
US-09-239-938-1
PCT-US55-00476-5
US-08-83-752-9
US-09-645-588-53
US-09-232-878-2
US-09-232-878-2
US-09-232-878-2
US-09-087-232-15
US-09-087-232-15
US-08-833-752-10
US-08-875-9674-4
US-08-875-9678-4
US-08-875-9678-4
US-08-875-9678-4
US-08-875-9678-4
US-08-875-9678-4
US-08-875-9678-4
US-08-875-9678-4
US-08-875-9678-4
US-08-875-968-1
US-08-875-968-1
US-08-833-752-8
US-09-045-583-54
US-08-833-752-8
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RESULT 4
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                                                                                   LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
                61 IKSMTDIXLLINLAISDLFFLLTVPFWAHYAAAQKDFGNTMCQLLFGLYFIGFFSGIFFII 120
                                                                  LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIR: 92660
COMPUTER READABLE FORM:
MEDIUM TYPER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
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                                                                                                                                                    181 HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                    Sequence 6, Application US/08833752
Patent No. 6448375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34,115
                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: VESSART, GILBERT
APPLICANT: LIBERT, FREDERICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,1
REFERENCE/TOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.8
Matches 215; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear; MOLECULE TYPE: protein US-08-833-752-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: CA
                                                                                                                                                                                                                                    US-08-833-752-6
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Patent No. 6133424.
GENERAL INFORMATION:
GENERAL TIPORATION:
APPLICANT: QUILILENT Et al.
TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                     APPLICANT: SAMSON, MICHEL
APPLICANT: PARMONTIER, MARC
APPLICANT: VASSART, GILBERT
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII
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100.0%; Pred. No. 4.9e-86;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
FILING DATE: 9-APR-1997
                                                                                                                                                                                                                             ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 13, Application US/09087232A; Patent No. 6153431
; Sequence 4, Application US/08833752
; Patent No. 6448375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 34,115 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 184 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 85.4% Best Local Similarity 100.0° Matches 184; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Altman, Daniel E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-833-752-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                    U.S.A.
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COUNTRY: U.S
ZIP: 92660
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61 LKSWTDIYLLNIAISDLFFLLTVPFWAHYAAAQWDFGNTWCQLLTGLXFIGFFEGIFFII 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLYFIFGFYGNMLYILLILINCKR 60
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APPLICANT: Gray et al.
TILLE OF INVENTION: Chemokine Receptor Materials and Methods NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.4%; Score 958; DB 4; Length 352; 100.0%; Pred. No. 1e-85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                       UPERMING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CNTENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,105
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.0%; Pred. No. 1e-
Matches 184; Conservative 0; Mismatches
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PRIOR APPLICATION DUMBER: US 08/666,020
FILING DATE: 19-JUN-1996
CLASSIFICATION 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,319
FILING DATE: 13-APR-1994
ATTORREY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08575967A Patent No. 6265184
                                                                                                   E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 352 amino acids TYPE: amino acid STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                 USA
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US-08-575-967A-2
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                                 COUNTRY:
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APPLICANT: DENG, HONGKUI
APPLICANT: ELIMBER, WILFRIED
APPLICANT: ELIMBER, WILFRIED
APPLICANT: LANDAU, NATHANIEL R.
APPLICANT: LIU, RONG
TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
TITLE OF INVENTION: MARCHANGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGTFFII 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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                                                                                                                                         COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/087,232A
FILING DATE: 28 MAY 1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: AP 31115
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,057
FILIGO DATE: 30 MAY 1997
ATTORNEY/AGENT INFORMATION:
NAME: KOLE, LISA B.
REGISSERATION NUMBER: 35,225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 14, Application US/08861105; Patent No. 6258527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 408-2628
TELEFAX: (212) 765-2519
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 352 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                   New York
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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181 HFPY 184
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
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REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 52, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
                                                                                              NAME: Altman, Daniel E
REGISTRATION NUMBERS:
REFERENCE/DOCKET NUMBERS:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TYPE: amino acid
MOLECULE TYPE: protein
US-08-833-752-5
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TELEPHONE: (617)227-7400
                                                           CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 184; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
COUNTRY: USA
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181 HFPY 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLTIDRYLAVVHAVFALKARIVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
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APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FEDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature

CTHER INFORMATION: /- "88C amino acid sequence"

US-08-575-967A-2
                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/575,967A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: No. 6265184and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32918
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-485-1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6448375
                                                                                                                                                                                                                                                                                                               TELEFAX: 206-485-1662
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
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Best Local Similarity 100.0
Matches 184; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
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HFPY 184
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61 LKSWTDIYLLNIAISDLFFLLTVPFWAHYAAAQWDFGNTWCQLLTGLYFIGFFSGIFFII 120
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                                                                                                                                                                                                                                                                                                                                  121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                                                              1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
                                                                                                                                        1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILLILNCKR
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TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                          0; Gaps
85.4%; Score 958; DB 4; Length 352; 100.0%; Pred. No. 1e-85; tive 0; Mismatches 0; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR ADDITOT
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Sequence 2, Application US/08466343D
Patent No. 6025154
GENERAL INFORMATION:
APPLICANT: LI, YI
TITLE OF INVENTION: CHEMOKINE RECEP
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                          84.8%;
98.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 352 amino acids
                        Query Match 84.8
Best Local Similarity 98.9
Matches 182; Conservative
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US-08-466-343D-2
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Patent No. 6403767

GENERAL INFORMATION:

APPLICANT: GTAham, Gerard J. et al.

TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled

Heptahelical Receptor Superfamily and Uses
                                                                                                                                                                                                                     1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
                                                                                                                                                                                                                                                          1 MDYQVSSPIYDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
                                                                                                                                                                               0; Gaps
                                                                                                                                      Score 952; DB 4; Length 352;
Pred. No. 3.9e-85;
2; Mismatches 0; Indels
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COMPUTER READABLE FORM:
COMPUTER: FIOPPY disk
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: CAL MAIL - 2000
CLASSIFICATION: CURROWN>
PRIOR APPLICATION NUMBER: 09/045,583
FILING DATE: CONKNOWN>
APPLICATION NUMBER: 09/045,583
FILING DATE: CONKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: MNI-044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-534-185-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPRONE: (617) 227-7400
TELEPAX: (617) 724-214
INFORMATION FOR SEQ ID NO: 52:
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LENGTH: 352 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Massachusetts
COUNTRY: USA
                                                                                                                                        84.8%;
98.9%;
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CORRESPONDENCE ADDRESS:
: 352 amino acids
amino acid
                                                                                                                                                         Best Local Siminaring .... Matches 182; Conservative
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                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-045-583-52
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                                                                                                                                                       Similarity
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181 HFPY 184
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                                                                                                                                      Query Match
Best Local &
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                                                                                                                                                                        61 LKSMTDIYLLNLAISDLFFELLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
                                                                                                                                                                                                  61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
                                                                                     1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILLLINCKR 60
                                                                                                               1 MDYQVSSPIYDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILLLINCKR 60
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                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN CHEMOKINE RECEPTOR HDGNR10 (AS AMENDED)
    Length 352;
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                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NOMBER: US/08/466,343D CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
TELECOMMUNICATION INFORMATION:
Score 952; DB 4;
Pred. No. 3.9e-85;
2; Mismatches 0
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59 KRLKSMTDIYLLINLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 IILLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MDYQVSSP--IYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINC 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN CHEMOKINE RECEPTOR HDGNR10 (AS AMENDED)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 69.2%; Score 776; DB 4; Length 354; Best Local Similarity 79.0%; Pred. No. 5.3e-68; Matches 147; Conservative 17; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION UNDER: 35,688
REFERENCE/DOCKET UNDER: 1488.1150000/EKS/KLM
TELECOMMUNICATION INFORMATION:
SOFTWARE: MICROSOFT WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,984A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/466,343D FILING DATE: 06-UUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                       ATG50023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : Sequence 9, Application US/08466343D
; Patent No. 6025154
                                                                                                                                                                            NAME: William T. Han
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATGS
TELECOMUNICATION INFORMATION:
TELEPRONE: 610 270 5024
TELEFAX: 610 270 5090
                                                          October 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                      FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: LI, YI
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | |||:
181 SPHFPH 186
                                                                                                                                                                                                                                                                                                                                                          TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                               Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 SSHFPY 184
                                                          FILING DATE: OC
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                                                                                                                                                                                                                       Sequence 5, Application US/09517605
Patent No. 6391567
GENERAL INFORMATION:
APPLICANT: Kwon, Douglas S.
APPLICANT: Kwon, Douglas S.
APPLICANT: Was Kooyk, Yvette
APPLICANT: Was Kooyk, Yvette
APPLICANT: Was Geijfenbeck, Tneo
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
TITLE OF INVENTION: CELLS
FILE REFERENCE: 1049-1-017
CURRENT APPLICATION NUMBER: US/09/517,605
CURRENT PILING DATE: 2000-03-02
                                 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LKSMTDIYLLINLAISDLFFLLIVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFYGNMLVILILINCKR 60
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Patent No. 638855
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: No. 6388055el Mouse Genomic Clone of the CC-
TITLE OF INVENTION: CRES Receptor
TITLE OF INVENTION: S. 5
CORRESPONDENCE ADDRESS:
ADDRESSES:
ADDRESSES: SmithKilne Beecham Corporation
STREET: 709 Swedland Road, P.O. Box 1539
CORR. King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
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MEDIUM IYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 83.4%; Score 936; DB 4;
Best Local Similarity 97.3%; Pred. No. 1.4e-63;
Matches 179; Conservative 3; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: DISAR
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181 HFPY 184
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181 HFPY 184
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US-08-724-984A-2
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                                                                                                                                                                                                     US-09-517-605-5
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            121
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Gaps ñ

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70 INLAISDLFFILITVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129
                                                                                                                                 70 INLAISDLFFLLIVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 FDZDY--GAPCHKFDYKQIGAQLLPPLYSLVFIFGFYGNMLVYLILINCKKLKCLTDIYL 81
                                                          10 YDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYL
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                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 VVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFP 183
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.9%; Score 694; DB 1; Length 360; 75.9%; Pred. No. 5.1e-60; Live 17; Mismatches 23; Indels
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995
       ; Pred. No. 4.9e-60;
17; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UCAL-237/02US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08450393A Patent No. 5707815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CSCTT. LUADD
RECIETRATION NUMBER: 31,822
REFERENCE/POCKET NUMBER: UCAL.
FELECOMMUNICATION INFORMATION:
TELEPAX: 415-883-5165
TELETAX: 380816COOLEYPA
INFORMATION FOR SED ID NO: 4:
       75.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 360 amino acids
amino acid
                       132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein US-08-450-393A-4
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     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 94306-2155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 132; Conserv
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                     Matches
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                                                                                                                                                                                                                                                                                                                                                                             10 YDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYL 69
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 VVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFP 183
                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                          Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 347;
                                                                                                                                                                                                                                           23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: STUART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R.
APPLICANT: Y1, Li
APPLICANT: Ruben, Steven M.
APPLICANT: Rosen, Cralg A.
ITILE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NOMBER: 0S/08/461,244
ELING DATE: 05-001/1995
CLASSIFICATION: 536
                                                                                                                                                                                                      61.9%; Score 694; DB 3; 75.9%; Pred. No. 4.9e-60; tive 17; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.9%; Score 694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 325800-445 FELECOMMUNICATION INFORMATION: TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08461244 Patent No. 5776729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 Becker Farm Road
(202) 371-2600
             TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 347 amino acids
                                                                                                                                                                                                      Query Match
Best Local Similarity 75.99
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201-994-1744
                                                                                                            single
                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
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STATE: New Jersey
                                                                                          TYPE: amino acid
STRANDEDNESS: Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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TELEPHONE:
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Search completed: June 3, 2003, 19:25:10 Job time: 32.4634 secs

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June 3, 2003, 19:17:26 ; Search time 55.061 Seconds (without alignments) 520.312 Million cell updates/sec
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1122
1 MDYQVSSPIYDINYYTSEPC.....AACHGHLLLGNPKNSASVSK 215
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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**Side Stage /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:

A_Geneseq_101002:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Thactive himan Oct	HIV-1 co-recentor	Inactive human CCR	Himan CRF Homo	Himan chemokine re	Himan C chemokine	HTV-1 CO-recentor	Non-endodenous hum	אוווי מוסיניסעריי היסינים אווייי	Buman BIV-1 co-rec
SUMMARIES ID	AAW27408	AAW88238	AAW27406	AAW27407	AAW27123	AAW23835	AAW88232	ABB56342	AAG80111	AAB82948
рв	18	20	18	18	18	19	50	22	22	22
* Query Match Length DB ID	215	215	184	352	352	352	352	352	352	352
% Query Match	100.0	100.0	85.4	85.4	85.4	85.4	85.4	85.4	85.4	85.4
Score	1122	1122	958	928	958	958	958	928	958	958
Result	7	7	3	4	5	છ	7	œ	σ	10

Human G-protein ch	ט פ	CCR5 prote				chemokine		_	T :		G-protein	G-protein	G-protein	G-protein	G-protein	acid seque		Human chemokine re			monocyte	Monocyte		0	Human wild-type CC	Human monocyte che	Human CCR2a profei	Human MCP-1 recept	⊆	Human MIP-1 alpha/	MIP-1		Rat CC chemokine r	Chemokine receptor
AAE07039	AAE07048	AAB83354	AAE04321	AAB46858	AAU97152	ABB08343	AAM52828	AAY41280	AAW23834	AAM52829	AAW07602	AAY80128	AAE07037	AAE07046	AAU97150	AAG79089	AAW27125	AAW26766	AAW54037	AAU07613	AAR79166	AAW35833	ABB56340	AAG80108	AAU07614	AAR79165	AAG80107	AAB46859	AAR52749	AAW26588	AAW25751	AAB20571	AAW29179	AAR99274
22	22	22	22	22	23	23	23	20	13	23	18	21	22	22	23	22	18	18	19	22	16	18	22	22	22	16	22	22	15	18	18	21	18	17
352	352	352	352	352	352	352	352	439	371	352	352	352	352	352	352	352	352	332	354	360	360	360	360	360	360	374	374	329	355	355	355	355	355	360
85.4	85.4	85.4	85.4	85.4	85.4	85.4	85.4	85.4	84.9	84.8	84.0	84.0	84.0	84.0	84.0	83.4		74.8	69.3	61.9	61.9	61.9			-:				۳,	53.3	ъ,	53,3	20.4	48.8
928	928	928	928	928	928	958	928	928	953	952	943	943	943	943	943	936	933	839	176	695	694	694	694	σ	694	694	9	608.5	298	298	298	ഹ	S)	•
11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	78	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

AAW2 XX C C C C C C C C C C C C C C C C C C	AAW27408 XX XX XX XX XX XX XX XX XX AW27408; XX
X & X	(EURO-) EUROSCREEN SA.
X	Libert F, Parmentier M, Samson M, Vassart G;
DR	WPI; 1997-479829/44.

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us-09-938-703-6.rag

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LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is the amino acid sequence of a CCR5 variant protein, designated CCR5-delta32, that includes the first 4 transmembrane domains 6 wild-type CCR5 (see AAM88232), but lacks transmembrane domains 5-7. CCR5 serves as a co-receptor for infection by macrophage-tropic (M-tropic) strains of HIV-1. Individuals the macrophage-tropic (M-tropic) strains of HIV-1. Individuals infection, but heterozygous individuals are susceptible. The infection, but heterozygous individuals are susceptible. The invention additionally relates to the identification of variant CCR5. The detection of CCR5 variants may be used to identify individuals at lower risk of infection relative to the general population who, if infected, may exhibit slower progression to AIDS. Probes and primers (see AAW84127-35) are provided for use in method is provided for inhibiting HIV-1 infection of a ceil expressing the CCR5 receptor. This involves introducing a nucleic acid encoding a CCR5 molecules present on the cell surface.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDYQVSSPIYDINYYISEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLYILILINCKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inactive, human Cys-Cys chemokine receptor-5; CCR5; human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2; predisposition; resistance; diagnosis; treatment; prevention; inflammatory disease: rheumatoid arthritis; glomerulonephritis; asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer; atherosclerosis; autoimmune disorder.
                                                                                                                                                                                                   New CCR5 variant protein of the HIV-1 co-receptor - useful in developing resistance of CCR5-expressing cells to HIV-1 infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 1122; DB 20; Length 215; Best Local Similarity 100.0%; Pred. No. 1.4e-125; Matches 215; Conservative 0; Mismatches 0; Indels 0;
                                                                                               Braun J, Quillent C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215
                                                  (MOND-) FOND MONDIALE RECH & PREVENTION SIDA,
                                                                                                                                                                                                                                                                   Disclosure; Page 38-39; 55pp; English.
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                                                                                               Beretta A,
      97US-0048057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                          Arenzana Siesdedos F,
                                                                                                                                   WPI; 1999-059835/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 AA;
      30-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLYFIFGFVGNALYILILINCKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                   The present sequence is an inactive human CC (Cys-Cys) chemokine receptor 5 (CYS5), which lacks the last 3 transmembrane regions and the regions involved in G protein-coupling. CCR5 or its CDNA can used to diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatorid arthritis, qionerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis, viral infections, especially human immunodeficiency virus type 1 or type 2 (HIV-1 or HIV-2) infection, cancer, atheroscierosis and autoimmune disorders. Subjects that express the inactive receptor have a predisposition, or resistance to HIV-1 and/or HIV-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCR5; CCR5-delta32; co-receptor; infection; diagnosis; AIDS;
                                    Active and inactive forms of human CC chemokine receptor CCR-5 useful to diagnose, prevent and/or treat inflammatory disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 1122; DB 18; Length 215; Best Local Similarity 100.0%; Pred. No. 1.4e-125; Matches 215; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 HFPYIKDSHLGAGPAAACHGHLLLGNPKNSASVSK 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "transmembrane domain 4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIV-1 co-receptor CCR5 variant CCR5-delta32
                                                                                    autoimmune disease and viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
32..56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW88238 standard; Protein; 215 AA.
                                                                                                                          Claim 7; Fig 1d-e; 94pp; English.
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/note= "t
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                                                                                                                                                                                                                                                                                                                                                                                                             215 AA;
N-PSDB; AAT90118.
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RESULT 2

Domain Domain

Domain Domain

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Gaps

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LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
                                                                                                                                                                                                                                                                                                                                                                          The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5), which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but not by monocyte chemoattraatant protein 1 (MCP-1), MCP-2, MCP-3, interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha) chemokines. Active CCR-5 is also a receptor of human immunodeficiency virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its CDNA can used to diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis, growth glomerulonephiritis, asthma, idlopathic pulmonary fibrosis and psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer, atherosclerosis and autoimmune disorders.
                                                                                                                                                                                                                                                                                    Active and inactive forms of human CC chemokine receptor CCR-5 . useful to diagnose, prevent and/or treat inflammatory disorders, autoimmune disease and viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour; asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy; diagnosis; leukocyte trafficking;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 958; DB 18;
Pred. No. le-105;
                                                                                                                                                                                                                Vassart G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                Samson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW27123 standard; Protein; 352 AA.
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100.0%; Prer
0; F
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                                                                                                                                     96EP-0870102.
                                                                                                         97WO-BE00023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                               Libert F, Parmentier M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 184; Conservative
                                                                                                                                                                                   (EURO-) EUROSCREEN SA
                                                                                                                                                                                                                                           WPI; 1997-479829/44.
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                                                                                                                                                                                                                                                         N-PSDB; AAT90117
                  Homo saplens
                                             WO9732019-A2.
                                                                                                         28-FEB-1997;
                                                                                                                                     06-AUG-1996;
01-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LKSWTDIYLLHIALSDLFFLLTVPFWAHYAAAQWDFGNTWCQLLTGLYFIGFFGGFFFFIT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIEGFVGNMLYILLINCKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention; inflammatory disease; rheumatorid arthritis; glomerulonephritis; asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer; atherosclerosis; autoimmune disorder.
                                                                                                                                                                                                                                                                                                                                                      The present sequence is an inactive human CC (CVs-CVs) chemokine receptor 5 (CCR5), which is not a receptor of human immunodeficiency virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or tits CDNA can used to diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis, glomerulonephritis, astima, idiopathic pulmonary fibrosis and psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer, atherosclearosis and autolumnume disorders. Subjects that express the inactive receptor have a predisposition, or resistance to HIV-1 and/or HIV-2.
                                                                                                                                                                                                                                                                 Active and inactive forms of human CC chemokine receptor CCR-5 useful to diagnose, prevent and/or treat inflammatory disorders, autoimmune disease and viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.4%; Score 958; DB 18; L
100.0%; Pred. No. 4.4e-106;
.1ve 0; Mismatches 0;
                                                                                                                                                                                              Samson M, Vassart G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW27407 standard; Protein; 352 AA.
                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 1a; 94pp; English.
                                                                                      97WO-BE00023.
                                                                                                                 96EP-0870102
96EP-0870021
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                                                                                                                                                                                          Libert F, Parmentier M,
                                                                                                                                                              (EURO-) EUROSCREEN SA.
                                                                                                                                                                                                                       WPI; 1997-479829/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 AA;
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181 HFPY 1
Homo sapiens
                          WO9732019-A2
                                                                                    28-FEB-1997;
                                                                                                                 06-AUG-1996;
                                                                                                                                  01-MAR-1996;
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                                                        04-SEP-1997
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Length 352;

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121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                        This protein sequence comprises of a novel human macrophage-selective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion between HIV and a target cell
                                                                                                                                                                                                                                                                                        CC chemokine receptor 5; CCR5; G-protein coupled receptor; human immunodeficiency virus; HIV; CD4; AIDS; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                    .120
ce= "extracellular loop-1 (Claim 19)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "extracellular loop-2 (Claim 19)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "extracellular loop-3 (Claim 19)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Combadiere C;
                                                                                                                                                                                                                                                                                                                                                                                                     /label- I
/note- "transmembrane domain"
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note= "transmembrane domain"
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187..210
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/note= "transmembrane domain"
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                                                                                                                                                                                                                                                           Human CC chemokine receptor 5 (CCR5).
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Kennedy PE, Murphy PM;
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                     AAW23835 standard; Protein; 352 AA.
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/label= VII
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/label= VI
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                                                                                                                                                                                                                                                                                                                     transgenic animal.
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181 HFPY 184
                                                                   181 HFPY 184
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                                                                                                                                        RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This polypeptide sequence comprises novel human chemokine receptor 86. a 6 protein coupled receptor that is involved in leukocyte trafficking. Its amino sequence was deduced from a conna clone (AAT95161) isolated from a macrophage library. It shows 62% identity to CCCKRI. Chemokine receptor 88-28 (see AAW77114) has also been identified. 88C and 88-28 receptors and their polypeptide fragments can be produced in transformed host cells. The receptors, peptides comprising one or more of the extracellular or intracellular comprising one or more of the extracellular or intracellular receptor activities particularly ligand and 6 protein binding, and are potentially potentially useful in the treatment of are potentially useful in the treatment of atheroslerosis, rheumatoid arthritis, tumours, asthma, viral infection, AIDS, inflammatory conditions, pathological immune response, abnormal haematopoietic processes etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to modulate leukocyte tráfficking, e.g. for treatment of
inflammation, tumours, viral infections, autoimmune diseases, etc.
G protein coupled receptor; ligand; modulator; antibody; human.
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/label- Intracellular_domain 89..112
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|abel= Extracellular_domain
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125..145
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/label* Intracellular_domain
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                                                             location/Qualifiers
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950S-0575967.
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N-PSDB; AAT85161,
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RESULT 8
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          The Sequence of the state of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                             1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILLILNCKR
                                                                                                                                                                                                                                                                                                                                                                                  in wild-type CCR5,
   The sequence
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                                                                                                                                                                                                                                                                                              Length 352;
 receptor that has been designated CCR5.
                                                                                                                                                                                                                                                                                            Query Match 85.4%; Score 958; DB 19;
Best Local Similarity 100.0%; Pred. No. 1e-105;
Matches 184; Conservative 0; Mismatches 0;
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TGA (Stop) in CCr5m303"
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142..167
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275..30
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                                                                                                                                                                                                                                                           352 AA;
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HFPY 184
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61 LKSMTDIYLLNLAISDLFFTLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serves as a correction to infection by macrophage-tropic (M-tropic) strains of HTV-1. The invention relates to the identification of a CCRS variant (see AAM88231), designated CCRSA333, comprising the first two transmembrane domains of wild-type CCRS, our lacking transmembrane domains 3-7. The presence of the CCRSA33 variant with the wild type CCRS allels shows a positive correlation with resistance to infection with M-tropic HTV-1 strains, and may indicate slower progression of the disease. The detection of CCRS variants may be used to identify individuals at lower risk of infection relative to the general population who, if infected, may exhibit slower progression to AIDS. Probes and for detecting the presence of such variants. A method is provided for inhibiting HTV-1 infection of a cell expressing the CCRS or inhibiting HTV-1 infection of a cell expressing the CCRS or inhibiting HTV-1 infection of a cell expressing the CCRS or inhibiting HTV-1 infection of a cell expressing the CCRS or inhibiting HTV-1 infection of a cell expressing the CCRS or inhibiting HTV-1 infection of a cell expressing the CCRS or inhibiting HTV-1 infection of a cell expressing the CCRS or inhibiting HTV-1 infection of a cell expressing the CCRS or inhibiting HTV-1 infection of a cell expressing the CCRS or inhibiting HTV-1 infection of a cell expressing the CCRS or including HTV-1 infection of a cell expressing the CCRS or including HTV-1 infection of a cell expressing the CCRS or including HTV-1 infection of a nucleic acid encoding a CCRS molecules present on the cell surface.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New CCR5 variant protein of the HIV-1 co-receptor - useful in developing resistance of CCR5-expressing cells to HIV-1 infection
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0
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                                                                                                                                                                                                                                                                 Beretta A, Braun J, Quillent C;
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100.0%; Pred. No. 1e-105;
live 0; Mismatches 0;
                                                                                                                                                                                            (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
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Best Local Similarity 100.0
Matches 184; Conservative
                                                                                                                                                                                                                                                                 Arenzana Siesdedos F,
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                                                              29-MAY-1998;
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03-DEC-1998
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WO200172830-A2.
     Homo sapiens
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AAB82948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                             The invention relates to G protein-coupled receptors (GPCRS) for which the endogenous ligand has been identified. Non-endogenous constitutively activated versalons of known SPCRs are used in the invention for the direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists. Such agonists are useful as therapeutic agents for diseases or disorders associated with GPCRs. The present sequence is a non-endogenous version of a known human GPCR.
                                                                                                                                                                                          use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection; inflammation; autoimmune disease; metastasis; bronchial asthma; lupus; chronic bowel inflammation; rheumatoid arthritis; cytostatic; antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                           1 MDYQVSSPIYDINYYISEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                     Identifying agonists of G protein-coupled receptors (GPCRs) for udisease treatment, comprises contacting candidate compounds with
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                                                                                                                                                                                                                                                                                                                                                        Query Match 85.4%; Score 958; DB 22; Length 352; Best Local Similarity 100.0%; Pred. No. 1e-105; Matches 184; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                             Claim 1; Page 277-278; 394pp; English.
                                                                                                                                        Lin I;
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                                                                                                                                       Jehmann-Bruinsma K, Liaw CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antirheumatic; antiarthritic.
                                                                             )5-APR-2001; 2001WO-US11098
                                                                                               07-APR-2000; 2000US-195747P
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                                                                                                                   (AREN-) ARENA PHARM INC
                                                                                                                                                         WPI; 2001-648759/74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human CCR5 protein.
                                                                                                                                                                                                                                                                                                                                       352 AA;
                                                                                                                                                                                                          versions of GPCRs
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                                     WO200177172-A2.
         Homo sapiens.
Synthetic.
                                                         18-OCT-2001,
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This invention describes a novel diagnostic agent (A) comprising at least two different ligands (1) for receptors (II) that are implicated in disease. (A) are used for the diagnosis of tumors (especially colorectal or prostatic), organ rejection, inflammation and autoimmune diseases. Also inhibitors of (1) are used therapeutically against tumors (and their metastases), inflammation (particularly bronchial asthma or chronic bowel inflammation), or autoimmune diseases (rheumation arthur or chronic bowel endocrine, motor or urogenital systems or skin are affected, and bone marrow diseases. The products of the invention are chemokine derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which have cytostatic, antiinflammatory, antiasthmatic, immunosuppressive, dermatological, antirheumatic, antiarthritic. chemokines act on specific tumor and inflammatory cells through a constellation of chemokine receptors (R), which control migration and prolliferation of these cells. AAG80045-AAG80128 represent human chemokine fragments used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 IKSMIDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
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                                                                                                                                                                                                                                                                                                                                                               Diagnostic agent containing two or more receptor-specific ligands, useful for detecting tumors, inflammation etc., also therapeutic use of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILLLINCKR
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                                                                                                                                                                                                                                                      Heitland A, Spodsberg N;
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100.0%; Pred. No. 1e-105;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 10; 26pp; German.
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                                                       02-APR-2001; 2001WO-EP03708.
                                                                                                              31-MAR-2000; 2000DE-1016013.
                                                                                                                                                                                                                                                   Forssmann W, Adermann K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-DEC-2001 (first entry)
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                                                                                                                                                                  (IPFP-) IPF PHARM GMBH. (FORS/) FORSSMANN U.
                                                                                                                                                                                                                                                                                                          WPI; 2001-626256/72.
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HFPY 184
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HFPY 184

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel compounds comprising specific amino acids within CCR5 (HIV 1 co-receptor) amino terminal domain including negatively charged and two sulfated tyrosine residues is useful for treating HIV infection in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of human HIV-1 co-receptor CCR5.

Amino acids 2-18 in the N-terminal region of CCR5 comprise an HIV-1

Equipal Aminding site that determines the specificity of the
interaction between CCR5 and HIV-1 spl20. Post-translational
sulfation of the tyrosine residues in the CCR5 N-terminus is
consequent for spl20 binding and may critically modulate the
susceptibility of target cells to HIV-1 infection in vivo. The
invention provides claimed sulfated peptides (see AAB82947) that
control in this consequence of the core of the consequence of the core in this consequence of the consequence of the core of t
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CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1; infection; therapy; vaccine; anti-HIV-1.
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                                                                                                               Location/Qualifiers
2..18
/note= "binds to HIV-1 gp120"
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                                                                                                                                                                                                                                                                                                                                                        29-FEB-2000; 2000US-185667P.
19-MAY-2000; 2000US-205839P.
07-FEB-2001; 2001US-267231P.
                                                                                                                                                                                                                                                                                                            28-FEB-2001; 2001WO-US06699
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Best Local Similarity 100.0
Matches 184; Conservative
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                                                                                                                                          Binding-site
                                                                       Homo sapiens
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The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10

CC ramellorating a disease or disorder associated with inflammation,

C amellorating a disease or disorder associated with inflammation,

defective or aberrant chemotaxis of immune cells, HIV infection (such as

CC defective or aberrant chemotaxis of immune cells, HIV infection (such as

Debrrant T-cell antigen presenting cell interaction. The disease or

CC disorder may also be an infection, a cytomegalovitus infection such

as an early stage HIV infection, a cytomegalovitus infection such

cc disorder may also be an intection, a cytomegalovitus infection such

as an early stage HIV infection, a cytomegalovitus infection such

cc disorder may be associated

CC disorder may be associated

cc neurodegenerative disorder. The disease or disorder may be associated

with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5

cis used as a food additive or preservative to increase or decrease

ctorage capabilities. CCR5 HDGNR10 DNA are useful for chromosome

clantibodies, agonists and antagonists are also useful in the

chaquosis, treatment and prevention of cancer (breast, ovary, adrenal

cuogenital); immune disorders (Addison's disease, allergies, autoimmune

cc disease, multiple sclerosis, rheumatoid arthritis and ulcerative

colitis); cardiovascular disorders (myocardial ischaemias) and
                                                                                                                                                                                                                 Human, G-protein chemokine receptor; CCR5; HDCNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; yctostatic; immunosuppressive, noctropic; neuroprotective, gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; pastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative collitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acid encoding a human G-protein chemokine receptor (CCR5) HOXMIO polypeptide, useful for preventing or treating autchimnune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.
                                                                                                                                                                          Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 40; Page 486-487; 495pp; English.
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                                       AAE07039 standard; Protein; 352 AA.
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22-SEP-2000; 2000US-0234336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                  (first entry)
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N-PSDB; AAD13198.
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RESULT 11
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Dobbs S, Perros M,
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                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                      Query Match
Best Local 3
                                                                                                                                                                                                                                                                           Matches
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                                                                                                                         61 IKSWTDIYLLMIAISDLFFLLIVPFWAHYAAAQWDFGNTMCQLLIGLYFIGFFSGIFFII 120
                                                                                                            61 LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
                                                                                                                                                         LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                                                                                                                     The invention relates to human G-protein chemokine receptor (CCR5) HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are useful for treating, preventing or ameliorating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune
                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                           Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV, human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive; noctropic; neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone masrow; pastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative collitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.
                                                                              1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid encoding a human G-protein chemokine receptor (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
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                                                                                                                                                                                                                                                                                                                                                      Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
                      Length 352;
                                             Indels
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                      Score 958; DB 22;
Pred. No. 1e-105;
             85.4%; SCC...
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                   AAE07048 standard; Protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-FEB-2000; 2000US-0181258.
09-MAR-2000; 2000US-0187999.
22-SEP-2000; 2000US-0234336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-FEB-2001; 2001WO-US04153.
                                                                                                                                                                                                                                                                                                                               (first entry)
                                           Matches 184; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA, Roschke V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-488966/53.
                               Best Local Similarity
352 AA;
                                                                                                                                                                                                                          HFPY 184
                                                                                                                                                                                                    HFPY 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                          AAE07048;
Sequence
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                      Query Match
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AAE07048
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asrooma) or defective or aberrant T-cell antigen presenting cell interaction. The disease or disorder may also be an infectious disease (e.g. a viral infection such as an early stage HIV infection, a cytomegalovirus infection, or a poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The disease or disorder may be associated with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5 ingand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein is used as a food additive or preservative to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists are also useful in the disposis, treatment and prevention of cancer (breast, overy, adrenal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 LLTIDRYLAVVHAVFALKARTVTFGVVTSVIIWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
infection (such as Pneumocystis carinii pneumonia or Kaposi's
                                                                                                                                                                                                                                                                                                                                                                                                                                                        gland, bone, bone marrow, gastrointestinal tract, liver, luig, urogenital); immune disorders (Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colliis); cardiovascular disorders (myocardial ischaemias) and wound healing. The present sequence is human CCR5 HDGNR10 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5; human immunodeficiency virus; anti-inflammatory disease; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.4%; Score 95%; DB 22; 100.0%; Pred. No. 1e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Preu. ....
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12-JAN-2000; 2000GB-0000663.
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reporter gene r treatment of

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The present invention relates to a transformed mammalian cell that contains a gene encoding CD4, a construct encoding a reporter gene under the regulation of an human immuno deficiency virus (HTV) long terminal repeat (LTR) and that has been transduced with a vector encoding a human chemokine receptor (CRR) where the CD4 and the CKR are present on the cell surface of transformed mammalian cell. The invention is useful for identifying drugs or antibodies that interfere with the transformed ramanian cell of a dentifying a human chemokine receptor that facilitates the infection of a particular HTV strain into the transformed mammalian cell. Compounds chartcular HTV strain into the transformed mammalian cell. Compounds dentified can be used to treat cellular dysfunction and to prevent or combat HTV infection. The present sequence is a human chemokine receptor (CKR), CC-CKR-5 related protein. CC-CKR-5 is the principal cofactor for entry mediated by the envelope glycoproteins of primary macrophage-tropic entry mediated by the envelope glycoproteins of primary macrophage-tropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKSMTDIYLLNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HDGNR10; human; G-protein chemokine receptor; antiinflammatory; immunodulatory; anticoagulant; antiallergic; immunosuppressive; cytostatic; antiparasitic; antipsoriatic; antiheumatic; antiarthritic; vasotropic; gene therapy; haematopoiesis; wound healing; coagulation; anglogenesis; solid tumour; infection; leukemla; growth factor activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.4%; Score 958; DB 22; Length 352; 100.0%; Pred. No. 1e-105; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                  Transformed mammalian cell (I) that contains a CD4 gene, re and HIV LTR for identification of drugs and antibodies for
                                                                                                                                                  Ellmeier W, Landau NR,
                                                                                                                                                                                                                                                                                                                                                              Disclosure; Column 47-50; 37pp; English.
                                                                               CENT.
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                                                                             AARON DIAMOND AIDS RES
UNIV NEW YORK STATE.
    96US-0020043.
97US-0858660.
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(first entry)
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Best Local Similarity 100.
Matches 184; Conservative
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                                                                                                                                                                                               WPI; 2001-417127/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             352 AA;
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181 HFPY 184
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                                                                                                                                                                                                                        N-PSDB; AAD08577
    19-JUN-1996;
19-MAY-1997;
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                                                                                                                                                  Littman DR,
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04-MAY-2001
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AAB46858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method for defermining whether an agent is capable of modulating the interaction of chamotactic chamokine receptor 5 (CCR5) with gp120, comprising incubating the agent with CCRS and gp120 and determining whether the agent modulates the interaction, where gp120 and determining whether the agent modulates the interaction, where gp120 is associated with CD4, and where the interaction is a low affinity binding. The method is used to identify an agent capable of modulating the interaction of CCR5 with gp120. An agent identified by the method is used to prepare a pharmaceutical composition for the treatment of a disease or condition associated with CCR5 and gp120 interaction, to treat a subject with a disease or condition associated with CCR5 and gp120 interaction, not for preparing a pharmaceutical for treating human immunodeficiency virus (HIV). It can also be treat anti-inflammatory diseases. The method is commercially useful, amenable to high throughput cores.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKSWIDIYLLNLAISDLFFLLIVPFWAHYAAAQWDFGNIMCQLLIGLYFIGFFSGIFFII 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; transformed mammalian cell; CD4; reporter gene; translocation; human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy; chemokine receptor; CRR; cellular dysfunction; HIV infection; cofactor; CC-CKR-5; envelope glycoprotein; anti-HIV.
                                                                Determining if an agent can modulate CCR5-gpl20 interaction, comprises incubating the agent with CCR5 and gpl20 and determining if the agent modulates the interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 352;
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                                                                                                                                                                                                              This sequence represents the human CCR5 protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.4%; Score 958; DB 22;
100.0%; Pred. No. 1e-105;
ive 0; Mismatches 0;
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                                                                                                                                                               Claim 1; Page 110; 113pp; English.
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WPI; 2001-477088/52.
N-PSDB; AAF87099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352 AA;
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61

121 121 181

Sequence

Query Match

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AAE04321;

RESULT 14 AAE0432 US6258527-B1

Homo sapiens

21-MAY-1997; 20-MAY-1996;

10-JUL-2001

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Gaps ö us-09-938-703-6.rag

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r-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis; anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock; immunoglobulin E-mediated allergic reaction; rheumatoid arthritis; prostaglandin-independent fever; bone marrow failure; sarcoidosis; hyper-eosinophilic syndrome; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human G-protein chemokine receptor polypeptides and polynucleotides, useful for identifying (ant)agonists to the G-protein chemokine receptor -
                                                                                                                                                                                                                                                                                                                                                                                                 95US-0466343.
98US-0195662.
99US-0339912.
                                                                                                                                                                                                                                                                                                                                          29-NOV-2000; 2000US-0725285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-226317/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (RUBE/) RUBEN S M.
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                                                                                                                                                                                                                               US2001000241-A1
                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-1995;
18-NOV-1998;
25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LIYY/) LI Y.
                                                                                                                                                                          Homo sapiens
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plasmid, and fragments, analogs and derivatives of the polypeptide. The plasmid, and fragments, analogs and derivatives of the polypeptide. The products of the inventon have autiniflammatory, immunomodulatory, anticollegic, immunosuppressive, vulnerary, cytostatic, anticollegic, immunosuppressive, vulnerary, cytostatic, antiparasitic, anticollegic, immunosuppressive, vulnerary, cytostatic, antiparasitic, anticollegic, broad anticollegic antico This invention describes a novel receptor polypeptide (I) selected from (1) a fully defined 329 amino acid sequence (II) fully disclosed in the specification; and (ii) a polypeptide encoded by the CDNA contained in a Claim la; Page 15; 22pp; English.

Sequence 352 AA;

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61 LKSMTDIYLLNLAISDLFFLLTYPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFII 120
                                                                                                                                                           61 LKSWTDIYLLALAISDLFFLITVPFWAHYAAAQWDFGNTWCQLLIGLYFIGFFSGIFFII 120
                                                                                                                                                                                                          LLTIDRYLAVVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSS 180
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Query Match 85.4%; Score 958; DB 22; Length 352; Best Local Similarity 100.0%; Pred. No. 1e-105; Matches 184; Conservative 0; Mismatches 0; Indels
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181 HFPY 184

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sequence 22, Appl
Sequence 23, Appl
Sequence 15, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 5, Appl
Sequence 6, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 9, Appl
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Sequence 14, Appli
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Sequence 2, Appli
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Sequence 3, Appli
Sequence 2, Appli
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                                                                                  Sequence 11, Appl
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Sequence 7, Appli
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Sequence 1, Appli
Sequence 16, Appl
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                                                                Sequence 11, App.
                                            Sequence 11,
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olson & Bear
Drive 16th Floor
0 US-09-939-226-6
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0 US-09-938-703-11
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US-09-922-895-1
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ADDRESSER: Knobbe, Martens, Olson
STREET: 620 Newport Center Drive
CITY: Newport Beach
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APPLICATION WINEBR: US/09/938,719
FILING DATE: 24-Aug-2001
CLASSIFICATION: <u >classification:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 13, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
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VASSART, GILBERT
LIBERT, FREDERICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SAMSON, MICHEL
      COMPUTER READABLE FORM:
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ZIP: 92660
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                                                                                                                                                    (without alignments)
4506.655 Million cell updates/sec
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                                                                                                                              3, 2003, 18:49:55 ; Search time 4.22266 Seconds
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                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                              protein search, using frame_plus_n2p model
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US-09-939-226-13
US-09-938-703-13
US-09-938-719-6
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Maximum Match 100%
Listing first 45 summaries
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Alignment Scores:
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LIBERT, FREDERICK
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
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MEDIUM TYPE: Floppy disk
COMPUTER: THE PC COMPUTER: THE PC COMPUTER: THE PC COMPUTER: SOFTWARE: PATENT PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24 Aug-2001
CLASSIFICATION: CLASSIFICATION: 
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ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                 33,10000
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Matches:
Conservative:
Mismatches:
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                                                                         NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: «Unknown>
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
                                                                                                                                                            : LENGTH: 34 amino acids
: TYPE: amino acid
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-938-719-13
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 27-70LY-2000
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY AGENT INFORMATION:

NAME: Altuan, Daniel E

REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/09939226
Patent No. US20020110805A1
GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
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TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SALD RECEPTOR
                                                                                                                                                                                                                                                                          1 ATTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTC 60
                                                                                                                                                                                                                                                                                                     4 IlelyaAspSerHisLeuGlyAlaGlyProAlaAlaAlaCysHisGlyHisLeuLeuLeu 23
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COMPUTER: Inteppy title.

COMPUTER: Inteppy title.

COMPUTER: Inteppo compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOUTHARE: PATENTIN Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/938,703

FILING DATE: 24-Mag-2001

CLASSIFTCATION NUMBER: 09/626,939

FILING DATE: 2000-07-27

ATORNEY/AGENT INFORMATION:

NEATHER ALMEN, DAILE E

REGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER: 34,115

REFERENCE/DOCKET NUMBER: 34,115

INFORMATION FOR SEQ IN 00: 13:
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ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
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Matches:
Conservative:
Mismatches:
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TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 13;
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SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/09938703; Patent No. US20020110870A1
GENERAL INFORMATION: GENERAL PROPERTY SAMSON, MICHEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
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STRANDEDNESS: single
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Best Local Similarity:
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US-09-939-226-6
Sequence 6, Application US/09939226
Sequence 5. Application US/09939226
Sequence 6. Application US/09939226
Sequence 7. Application US/09939226
Sequence 6. Application US/09939226
Sequence 7. Application
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Sequence 6, Application US/09938703
Sequence 6, Application US/09938703
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
VASSART, GILBERT
LIBERT, FREDERICK
LIBERT, REDERICK
LIBERT, REDERICK
LIBERT, RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version #1.25 (EPO)
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                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: 18
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.

ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 6:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID 1
US-09-939-226-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Newport Beach
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Best Local Similarity:
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US-09-938-703-6
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LIBERT, ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
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ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 124-Mug-2001
FILING DATE: 24-Mug-2001
COMPAND: APPLICATION CURNOWD>
                  US-09-938-703-3_COPY_792_885 (1-94) x US-09-938-703-13 (1-34)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                   61 GGGAATCCTAAAACTCTGCTTCGGTGTCGAAA 93
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REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
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; TYPE: amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-938-719-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION UNDER: 09/626,939
FILING DATE: 27-7ULX-2000
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/09938719
Patent No. US20020106742A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARMENTIER, MARC
VASSART, GILBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SAMSON, MICHEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
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NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
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92.68%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
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AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTC 60
                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPOTER: TBM PC compatible
OPERATUG SYSTEM: PC-DOS/AKS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-938-703-3_COPY_792_885 (1-94) x US-09-938-703-6 (1-215)
                                                                                                ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
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Matches:
Conservative:
Mismatches:
Indels:
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,703
FILING DATE: 24 Aug-2001
CLASSIFICATION: <unstrainty-control of the control of th
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FILING DATE: 2000-07-27
ATTORNEY AGRAY INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Patent No. US2002016742A1
GENERAL TREORARION:
APPLICANT: SAMSON, MICHEL
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                                                                     CORRESPONDENCE ADDRESS:
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                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
                                                                                                                                                                                                                     STATE: CA
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US-09-938-719-11
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PARMENTIER, WARC
VASSARI, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 TIAAAGAIAGICAICIIGGGGCIGGICCIGCCGCIGCIIGICAIGGICAICIGCIACICG 61
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,719
FILMS DATE: 24-Aug-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILLNG DATE: 27-JULY-2000
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC_COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-938-703-3_COPY_792_885 (1-94) x US-09-938-719-11 (1-54)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37,000
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 GlylleLeuLysThrLeuLeuArgCysArgAsn 50
                                                                                                                                                                                                                                                                        NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE,DOCKET NUMBER: «Unknown>
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

RAPLICATION NUMBER: US/09/939,226
FILLING DATE: 24 ANG-2001

CLASSIFICATION: <URKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
US-09-939-226-11
Sequence 11, Application US/09939226
Patent No. US20020110805Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 54 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SAMSON, MICHEL
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
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Percent Similarity:
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                     Alignment Scores:
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US-10-232-686-2
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VASSARI, GILBERT
LIBERT, FREDERICK

LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE ACID MOLECULES ENCODING SAID RECEPTOR

AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                  20 LeuLysileValileLeuGlyLeuValLeuProLeuLeuValMetValileCysTyrSer 39
                                                                                                                                                                                                                                                                                                                                                                                                              2 TIAAAGAIAGTCAICITGGGGCIGGICCIGCCGCIGCITGICAIGGICAICTGCIACICG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: PATECHIIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         US-09-938-703-3_COPY_792_885 (1-94) x US-09-939-226-11 (1-54)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                              0000
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 GlylleLeuLysThrLeuLeuArgCysArgAsn 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 GGAATCCTAAAAACTCTGCTTCGGTGTCGAAAT 94
                             REFERENCE/DOCKET NUMBER: «Unknown»
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHRACTERISTICS:
LENGTH: 54 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/POCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                      Indels:
                                                                                                                                                TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 11:
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STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/09938703
Patent No. US20020110870A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 54 amino acids
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COMPUTER READABLE FORM:
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100.00%
100.00%
92.68%
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                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity: 1
Query Match: 9
DB:
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                                                                                                                                                                                                                         Alignment Scores:
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2 TTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTCG 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNRIO
FILE REFERENCE: 1488.11500N
CURRENT APPLICATION NUMBER: US/10/232,686
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: 09/339,912
PRIOR PILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR PLILING DATE: 1999-06-65
PRIOR PLILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PARCHAIN NUMBER: 08/466,343
PRIOR PLILING DATE: 1995-06-06
SOFTWARE: PARCHAIN NUMBER: 08/466
SOFTWARE: PARCHAIN VERSION 3.0
                                                                                                                                                                                        2 TTAAAGATAGTCATCTTGGGGCTGGTCCTGCCTGCTTGTCATGGTCATCTGCTACTCG
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US-10-086-814-1
Sequence 1, Application US/10086814
Sequence 1, Application No. US20030092632A1
SEREMAL INFORMATION:
APPLICANT: OLOGIC, Tatjana
APPLICANT: OLOGIC, Tatjana
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 61010-AB-1
CURRENT APPLICATION NUMBER: US/10/086,814
CURRENT FILING DATE: 2002-02-28
                                                                                                                                            US-09-938-703-3_COPY_792_885 (1-94) x US-09-938-703-11 (1-54)
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                                     Conservative:
Mismatches:
Indels:
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Mismatches:
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                                                                                                                                                                                                                                                                           62 GGAATCCTAAAAACTCTGCTTCGGTGTCGAAAT 94
                                                                                                                                                                                                                                                                                                 40 GlylleLeuLysThrLeuLeuArgCysArgAsn 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 GGAATCCTAAAAACTCTGCTTCGGTGTCGAAAT 94
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152.00
100.00%
100.00%
92.68%
               152.00
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92.68%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                       Best Local Similarity:
Query Match:
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US-09-725-285-2

) Sequence 2, Application US/09725285

) Patent No. US2001000241A1

) GENERAL INFORMATION:

| APPLICANT: Li, Yi
| APPLICANT: Ruben, Steven, M.

| TITLE OF INVENTION: GCR5 Receptor)

| TITLE OF INVENTION: GCR5 Receptor)

| TITLE OF INVENTION: US481.115.003

| CURRENT FILING DATE: 2000-11-29

| PRIOR APPLICATION NUMBER: US/09/725,285

| PRIOR PILING DATE: 1999-10-25

| PRIOR PILING DATE: 1998-11-18

| PRIOR PILING DATE: 1998-11-18

| PRIOR PILING DATE: 1996-11-18

| PRIOR PILING DATE: 1996-06-06

| WINGER OF SEQ ID NOS: 9

| SEQ ID NO 2

| SEQ ID NO 2

| SEQ ID NO 2

| SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
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Mismatches:
Indels:
Gaps:
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Matches:
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                                                                                                                                                               ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
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      STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYBOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                 152.00
100.00%
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Best Local Similarity:
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Best Local Similarity:
                                                                                                                                                                                                                        US-09-734-221A-14
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                                                                                                                                                                                                                                                                                                                 Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DENG, HONGKUI
ELLMEIER, WILFRIED
LIANDAU, NATHANIEL R.
LIANDAU, NONG
LIU, RONG
TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
MACKOPHAGE_TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 TIAAAGAIAGTCAICTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTCG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: David A. Jackson, Esq. STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION TO STATE TO STATE TO STATE TO STATE TO STATE TO STATE TO SOFTWARE TO S
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Matches:
Conservative:
Mismatches:
Indels:
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-004
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/09734221A
Publication No. US20030096221A1
GENERAL INFORMATION:
APPLICANT: LITTMAN, DAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID No: 14:
SEQUENCE CHRACTERISTICS:
TENGTH: 352 amino acid
TYPE: amino acid
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                    152.00
100.00%
100.00%
92.68%
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                              Alignment Scores:
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                                                                                     LENGTH: 352
TYPE: PRT
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US-09-779-879A-2

i Sequence 2, Application US/09779879A

i Sequence 2, Application US/09779879A

i Sequence 2, Application US/09779879A

i Settent No. US2002004876A1

i GENERAL INFORMATION:

i APPLICANT: Rosen, Craig A.

i APPLICANT: Li, Yi

i APPLICANT: Li, Yi

i APPLICANT: Huben, Steven, M.

i TITLE OF INVERTION:

i TITLE OF INVERTION:

i TITLE OF INVERTION:

i TITLE OF INVERTION NUMBER: US 60/1979, 879A

CURRENT FILING DATE: 2001-02-09

i PRIOR APPLICATION NUMBER: US 60/181, 258

PRIOR APPLICATION NUMBER: US 60/187, 999

PRIOR FILING DATE: 2000-03-09

i PRIOR PILING DATE: 2000-09-22

i PRIOR PILING DATE: 2000-09-22

i NUMBER OF SEQ ID NOS: 58

seq ID NO 2

i ENGRENT: BALCH OF SEQ ID NOS: 58

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i ENGRENT: APPLICATION VERSION 3.0
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Matches:
Conservative:
Mismatches:
Indels:
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Sequence 2, Application US/09759841
Fatent No. US20010039026A1
GENERAL INFORMATION:
APPLICANT: Rickett, Graham A
APPLICANT: Perrox, Manoussos
TILLE REFERENCE: PC10343APME
CURRENT PLILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US/09/759,841
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: GB 0000661.9
PRIOR APPLICATION NUMBER: GB 0000663.5
PRIOR FILING DATE: 2000-01-12
SEQ ID NO 2
LENGTH: 352
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100.00%
92.68%
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US-09-759-841-2
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US-09-779-879A-2
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Best Local Similarity:
Query Match:
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Q8R3C9
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196
30.2
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                                                                   June 3, 2003, 19:19:16; Search time 6.42683 Seconds (without alignments) 993.874 Million cell updates/sec
                                                                                                                                                                                                                       671580
         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                   US-09-938-703-6_COPY_185_215
164
1 IKDSHLGAGPAAACHGHILIGNPKNSASVSK 31
                                                                                                                                                                                                                   Fotal number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	075303 homo sapien	O9p1t8 homo sapien	09plt5 homo sapien	08te18 homo sapien	O8vt73 anabaena sp	09w5c7 drosophila	O8xnw7 clostridium	Ogaf65 clavibacter	0911d3 streptomyce	09a9q4 caulobacter	09les2 arabidopsis	094b29 arabidopsis	097fk0 clostridium	09w619 cynobs pyrr	08wzt3 neurospora	Q9p098 homo sapien
SUMMARIES		П	075303	O9P1T8	Q9P1T5	QSTEJ8	Q8YT73	Q9W5C7	Q8XNW7	Q9AF65	Q9L1D3	Q9A9Q4	Q9LES2	Q94B29	Q97FK0	Q9W619	Q8WZT3	Q9P098
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		Result No.	H	7	e	₹	Ŋ	9	7	80	6	10	11	12	13	14	15	16

RESULT 2 Q9P1T8

Q8F3C9 mus musculu Q9Cw46 mus musculu G64731 arabidopsis O40960 little cher Q9XYA3 sepla offic Q9XYA3 sepla offic Q9XYA3 sepla offic Q9XYA7 drosophila Q9QZp7 mus musculu Q9QZp7 mus musculu Q9QZp7 mus musculu Q9QZp7 mus musculu Q9117 streptomyce Q9YX7 drosophila Q59736 rhodobacter Q8Sqy1 encephalito Q8P3C homo saplen Q9pusa crocodylus Q9Pus phono saplen Q9pusa crocodylus Q9Pus Q9YMZ arabidopsis Q9bie6 leishmania Q9Yec5 drosophila Q9Yec5 drosophila Q9Yeb bovine aden Q65868 barley yell Q9V414 drosophila Q9V458 drosophila Q9Y458 drosophila Q8XTC0 ralstonia s	ALIGNMENTS ALIGNMENTS 11. 08, Created) 12. 08, Last sequence update) 13. 19, Last annotation update) 14. 19, Last annotation update) 15. 19, Last annotation update) 16. 19, Last annotation update 17. Chang G., Michael N.L.; 18. and Functional Characterization of the Complete 18. The Chemokine Receptor CCR-5, a Major Entry Co- 1944.11. 1944.11. 1947.11. 1948.11. 1948.11. 1948.11. 1948.11. 1948.11. 1948.11. 1948.11. 1948.11. 1948.11. 1948.11. 1948.11. 1948.11. 104. 105	1. BA416F7 CRC64; DB 4; Length 215; 3.9e-16; es 0; Indels 0; Gaps 0; 3.1
QBR3C9 Q9CW46 Q40960 Q9XYA3 Q9XYA3 Q9TUJ5 Q9TUJ5 Q9GP7 Q9GP7 Q9GP7 Q9GP7 Q9FXR7 Q9FXR7 Q9FXR7 Q9FXR7 Q9FXR7 Q9FXR7 Q9FXR7 Q9FXR7 Q9FXR8 Q9FXR8 Q9FYR8 Q9FYR8 Q9FYR8 Q9FYR8 Q9FYR8 Q9FYR9 Q9FYR8 Q9FYR8 Q9FYR8 Q9FYR8 Q9FYR9 Q9FYR8	ALIGNMENTS 1 1 3 075303 PRELIMINARY; PRT; 215 AA. 2075303 01-NOV-1998 (TrEMBLrel. 08, Created) 01-NOV-1998 (TrEMBLrel. 19, Last sequence update) 01-NOV-1998 (TrEMBLrel. 19, Last sequence update) 01-NOV-1998 (TrEMBLrel. 19, Last annotation update) 02-Chemokine receptor. 02-Chemokine receptor. 03-CC-Chemokine receptor. 03-CC-Chemokine (Humana). 03-CC-Chemokine (Humana). 03-CC-Chemokine Receptor (NOBI_TAXID=9606; 04-CC-CT-CT-CT-CT-CT-CT-CT-CT-CT-CT-CT-CT-	7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7
11111111111111111111111111111111111111	rnary; rel. 08, Cr rel. 08, Le rel. 19, L	PROTEIN_R 23946 MW; 100.0%; 100.0%; tive 0 AACHGHILL AACHGHILL
1996 1756 1756 1756 1756 1756 1756 1756 175	PRELIMINARY (TrEMBLE). (TrEMBLE). Freceptor.	0262; G_PROT 15 Aa; 2394 1arity 100 Conservative SHLGAGPAACH
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119 49 20 20 20 20 20 20 20 20 20 20	ALIGNME OUT 1 075303 PRELIMINARY; PRT; 2 075303 PRELIMINARY; PRT; 2 075303 PRELIMINARY; PRT; 2 01-NOV-1998 (TTEMBLrel. 08, Last seque 01-DEC-2001 (TTEMBLrel. 19, Last annot CC-chemokine receptor. CC-chemokine receptor. HOMO sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata Mammalia; Eutheria; Primates; Catarrhi NCBL_TAXID=9606; [1] SEQUENCE FROM N.A. Tse L., Ehrenberg P.K., Chang G., Mich Tse Lo, Commitce (UNV-1977) to the EMBL/GenBa EMBL, AF009962; AAC3944.1; - InterPro; IPRO00276; GPCR_Rhodpsn. PROSITE: PS00237; G PROMEIN RECEP F1 1	ACSITE; sceptor. SQUENCE / Match Local S nes 31
	RESULT O 7 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	C100 2E

178 AA.

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SEQUENCE FROM N.A.

MEDLINE-21595285; PubMed-11759840;

A RaneCo T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

A RaneCo T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

A RaneCo T., Irigucih M., Ishikawa A., Kawashima K., Kimura T.,

A Rishida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A.,

Rishida Y., Kohara M., Matsumoto M., Takazawa M., Yamada M.,

Tawuda M., Tabata S.,

"Complete genomic sequence of the filamentous nitrogen-fixing

"Complete genomic sequence of the filamentous nitrogen-fixing

"Complete genomic sequence of the filamentous nitrogen-fixing

"Tyanobacterium Anabaena sp. strain PCC 7120.";

DNA Res 8: 8:205-213(2001).

"BMBL; APO03591; BAB4552.1;

"RiterPro; IPR001509; Epimerase_Dh.

"RiterPro; IPR001205; NAD binding."
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jikuya H., Takano J., Momura N., Kikuno R., Nagase T., Ohara O., "The nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                                                                                                                      Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 33.5%; Score 55; DB 4; Length 178; Best Local Similarity 50.0%; Pred. No. 3.3; Matches 12; Conservative 1; Mismatches 5; Indels
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBL_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK074125; BAB84951.1; -.
NOW_TER 1 1
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                                                                01-00N-2002 (TEMBLrel. 21, Created)
01-JUN-2002 (TEMBLrel. 21, Last sequence update)
01-JUN-2002 (TEMBLrel. 21, Last annotation update)
FLJ00197 protein (Fragment).
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01-MAR-2002 (TIEMBLREL. 20, Last sequence update)
01-JUN-2002 (TIEMBLREL. 21, Last annotation update)
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TIGRFAMS; TIGR01179; galE; 1.
          PRELIMINARY;
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
MEDLINE-99392755; PubMed-10465086;
Aikhionbare F.O., Newman C., Womack C., Roth W.W., Stringer H.G. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99392755; PubMed-10465086;
Alkhionbare F.O., Newman C., Womack C., Roth W.W., Stringer H.G. Jr.,
Bond V.C.;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Characterization of a third CCR5 amplicon from CCR5-delta32-
heterozygous HIV-1-infected individuals.";
AIDS 13:1585-1586(1999)
EMBL; AF052244; AAF05577.1; -.
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Pred. No. 9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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DAEB2A5A9529C3A9 CRC64;
                                                   01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Mutant chemokine receptor CCR5 (Fragment).
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100.0%; Pred. No. ...
33 A.A.
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PRT;
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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41 41
52 AA; 5962 MW;
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
ACCOCCOS DET THE SET T
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336 AA.

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Gaps

9

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                                                                        Gaps
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0
                            Y Match 33.5%; Score 55; DB 16; Length 336; Local Similarity 35.5%; Pred. No. 6.3; hes 11; Conservative 7; Mismatches 13; Indels
336 AA; 36733 MW; 5C4E7F6F6E855276 CRC64;
                                                                                                                        1 IKDSHLGAGPAAACHGHLLLGNPKNSASVSK 31
                                                                                                                                                                                  RESULT 6
Q9W5C7
                                                                                                                                 g
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RESULT 4 Q8TEJ8

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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                             Probable exonuclease.
                                                                                                                                                                                                                                                                                                       STRAIN=13 / TYPE A;
PubMed=11792842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 727 AA;
                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                         NCBI_TaxID=1502;
                                                                     CPE0215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cellulase CelA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             flesh-eater."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268
                                                                        SECD OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09AF65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09AF65
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      DE GRANDE BERNAR BERNAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Manatiddes P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Morthan J.R., Yandell M.D., Shang Q., Chen L.X.,
Sutton G.G., Morthan J.R., Yandell M.D., Shang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barllew R.M., Basu A., Baxendale J., Bayraktarodyl L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolishakov S.,
RA Beeson K.Y., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
Ra Cherry J.M., Cawley S., Dalhke C., Davenport L.B., Davies P.,
Buttis K.C., Buchen M.R., Bouck J., Brokstein P., Brottler P.,
Buttis K.C., Gabriellan A.E., Garg N.S., Center I.W., Glasser K.,
RA Buttis R.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Rodson K.J., Edwicky D., Helman T.J., Hernandez J.R., Houck J.,
Rad Glock A., Goog F., Gorrell J.H., Gu Z., Gann P., Harris M.,
RAIUSh F., Karpen G.H., Kazit C., Kravitz S., Kulp D., Lai Z.,
Jalali M., Kalush F., Karpen G.H., Will W. H., Iboywe J. Lia X.,
Rask D., Hostinn N.V., Morbary C., Morris J., Mosherfi A.,
Moutt S.M., Moy H., Murphy B., Murphy L., Muzny D.M., Nelson D.I.,
Relazolo M., Pittman G.S., Pan S., Pollard J., Weilson D.I.,
Radson D.M., Pittman G.S., Pan S., Pollard J., Weilson B.,
Radson K., Raseranan D.A., Stapleton M., Stupsk M.P., Rang X.,
Rad R. K., Rodges R.W., Shong W., Zhong W., Stubs R.,
Spier E., Spradling A.C., Stapleton M., Stupsk M.P., Weissenband J.,
Rheng X.H., Zhong F.N., Rubing G.M., Weissenband J.,
Rheng X.H., Zhong F.N., Rubing G.M., Weissenband J.,
Rheng X.H., Zhong F.N., Rubing G.M., Weissenband J.,
Rheng K.H., Zhong F.N., Rubing G.M., Venter J.C.,
Rheng K.H., Zhong F.N., Rubing G.M., Weissenband J.,
Rheng K.H., Zhong F.N., Rub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28602 MW; 9F10B77DE62EA3A7 CRC64;
                                                                                                                                Last annotation update)
                                                                                                    Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
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276 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              407 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                 Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'lyBase; FBgn0029537; CG14633.
                                                    01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Conservative
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 GAGPAAAC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                               Ephydroidea; Dros
NCBI_TaxID=7227;
                                                                                                                                                            CG14633 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OBXNW7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8XNW7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
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Gaps
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                                                                                                                                                                                                         Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clavibacter michiganensis subsp. sepedonicus.
Actinobacteris; Actinobacteria; Actinobacteridae;
Actinomycetales; Micrococcineae; Microbacteriaceae; Clavibacter.
NCBL_TAXID-31964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laine M., Haapalainen M., Wahlroos T., Kankare K., Nissinen R., Rasswal S., Metzler M.C.;
Rasswal S., Metzler M.C.;
"The cellulase encoded by the native plasmid of Clavibacter michiganensis subsp. sepedonicus plays a role in virulence and contains an expansin-like domain.";
Physiol. Mol. Plant Pathol. 0:0-0(2001).

EMBL; ANO0731; BAK16222.1;
HSSP; P54583; IECE.
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Clostridium perfringens.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.9%; Score 54; DB 16; Length 407; 38.5%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 2; Length 727; . 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Exonuclease; Complete proteome.
SEQUENCE 407 AA; 46819 MW; 5E71E267DDC8B4A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLYCOSYL_HYDROL_F5; UNKNOWN_1.
; 75811 MW; 96DF9B664873985D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-UUN-2001 (TIEMBLrel. 17, Created)
01-JUN-2001 (TIEMBLrel. 17, Last sequence update)
01-JUN-2002 (TIEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).

EMBL; AP003185; BAR79931.1; -.

Interpro; IPR004843; M-ppestrase.

Interpro; IPR004844; S/T_phosphtse.

Interpro; IPR004593; SboD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          727 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 11;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 54;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 LGAGPAAACHGHLLLGNPKNSASVSK 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001919; Bac_celose-bind.
InterPro; IPR001547; GH_5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAAACGSHLLVTGPKGTVRV 588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00149; Metallophos; 1.
TIGREAMS; TIGR00619; sbcd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00553; CBM_2; 1.
Pfam; PF00150; cellulase; 1.
PROSITE; PS00659; GLYCOSYL_H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.9%;
52.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 38.5%;
hes 10; Conservative
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Best Local Similarity 52.4%,
"Thes 11; Conservative
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us-09-938-703-6_copy_185_215.rspt

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Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TIEMBLEAL 15, Created)
01-OCT-2000 (TIEMBLEAL 15, Last sequ
01-JUN-2002 (TIEMBLEAL 21, Last anno
                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                              3 DSHLGAGPAAACHGHLLLGN 22
      32.3%;
55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Arabidopsis cDNA clones.";
   Query Match 32.3'
Best Local Similarity 55.0'
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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MEDLINE-21173698; PubMed-11259647;
MEDLINE-21173698; PubMed-11259647;
Mistrman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Blsen J., Heidelberg J.F., Alley M.R.K., Ohla N., Maddock J.R.,
Pottocka I., Nelson W.J., Newton A., Stephens C., Phadke N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Todonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-A3(2) / M145;

STRAIN-A3(2) / M145;

Hentley S.D., Chater K.F., Cerdeno Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quall N.A., Kleser H.,

Harper D., Bateman A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                              Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinomycetaceae; Streptomycineae; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 41:141-147(12002).
EMBL; ALIS7953; CAB76068.1; -.
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Pred. No. 12;
0; Mismatches 3; Indels
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PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
Hypothetical protein; Complete proteome.
SEQUENCE 499 AA; 54933 MW; CCF42A7FB833CEAF CRC64;
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312 AA; 32324 MW; A9E75F8CIDCE1C9F CRC64;
                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
910-DUN-2002 (TrEMBLrel. 21, Last annotation update)
SCO1549 OR SCIII.05C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                            312 AA.
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76.9%;
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CC0920.
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                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caulobacter crescentus
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                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-1902;
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                      Q9L1D3
Q9L1D3;
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Q9A9Q4
09L1D3
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 51.4 kDa protein (AT3956860/T8M16_190) (UBP1 interacting
                                                                                                                                                                                                                                                                                                                                                                     TBMIG...1900 OR AT3G56860 OR UBA2A.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Shinn P., Tracy S.E., Banh J., Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Haysahizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nauyen M., Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M., Seki M., Seki M., Seki M., Saturai T., Satou S., Sakano H., Sakurai T., Satou G.C., Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dengales, Engan M.C., Chan M.M., Chang C.H., Chang E., Dale J.M.,
Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
Tang C., Toriumi M., Wu H.C., Yanamurz Y., Yu G., Bowser L.,
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
Ramiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
Sakurai T., Satou M., Skinn P., Southwick A., Shinozaki K.,
Davis R.W., Ecker J.R., Theologis A.,
"Arabidopsis Full Length CDNA Clones.";
Submitted (WAR-2002) to the EMBL/GenBank/DDBJ databases.
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,
Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,
Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,
Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,
Parabidopsis cDNA Clones.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1] SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Benes V., Wurmbach E., Drzonek H., Ansorge W., Mewes H.W., Rudd S.,
Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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  Length 499;
                                           8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EU Arabidopsis sequencing project;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DB 16;
19;
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                                      1; Mismatches
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408 AA

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Created)
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Best Local Similarity 45.0%;
--hoa 9; Conservative
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18,
                                                                                                                                                                                                                  Clostridium acetobutylicum.
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                                                              PRELIMINARY;
                                                                                                       (TrEMBLrel.
                                                                                                                                                                   DNA repair exonuclease.
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                    NCBI_TaxID=1488;
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                                                                                                          01-OCT-2001
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Hypotherical 51.4 kDa protein.
18M16_190 OR AT3656860.
Arabidopsis thaliana (Mouse-ear cress).
Rukaryork; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SUCTURICA A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
Southwich A., Karlin-Neumann G., Nguyen M., Lam B., Chen H.,
Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Ecker J., Theologis A., Davis R.W.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY04288; AAK6852.;
EMBL, AY04288; AAK6852.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE A., Lam B., Miranda M.,
NGUYED M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
Palm C.J., Bowser L., Jones T., Bahh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Marusaka M., Pham P.K., Sakano H.,
Kim C., Lin J., Satou M., Sahin P., Yamada K., Shinozaki K.,
Sakurai T., Shoologis A., Davis R.W.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                DB 10; Length 478;
multifunctional effector of pre-mRNA maturation in plants.";
                                                                                                                                                                                                                                                                                                                                                                          7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   478 AA; 51440 MW; 0EDIC8FBA231E1E6 CRC64;
                                                                                                                                                                                                                                                                    .l protein.
478 AA; 51439 MW; 0CD3653669BE2DA4 CRC64;
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; Pred. No. 21;
4; Mismatches
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PROSITE; PS50102; RRM; 2.
PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
                                                                                                                                                                                                                        PROSITE; PS50102; RRM; 2.
PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
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                MO1. Cell. Biol. 0:0-0(2002).

EMBL, A0390921; AAK5946.1;

EMBL, A703746; AAK5946.1;

EMBL, A7031040; AAK5966.1;

EMBL, A7991040; AAK56269.1;

EMBL, A7991040; AAM13861.1;

InterPro; IPR000504; RNA_rec_mot.

Fiam; PF00076; rrm, 2.

SMART; SM00360; RRM; 2.
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                                                                                                                                                                                                                                                                                                                                32.0%;
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                       Hypothetical
SEQUENCE 47
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XX MEDLINE-21359325; PubMed-11466286;

XR MEDLINE-21359325; PubMed-11466286;

XR Gibson R., Ereton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

RA Gibson R.L., Sabathe F., Doucette-Stamm.L., Soucaille P., Daly M.J.,

RA Gibson R.L., Sabathe F.V., Smith D.R.;

RA Gibson R.L., Sould E.V., Smith D.R.;

RA Gibson R.L., Sabathe F.V., Smith D.R.;

RA Gibson R.L., Soucaille P., Daly M.J.,

RA Gibson R.L., Sabathe F.V., Smith D.R.;

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RA Gibson R.L., Suphosphise.

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
NCBI_TaxID-8330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUB-RECENTED LIMB BLASTEMA;
Shimizu-Nishikawa K., Tazawa I., Uchiyama K., Yoshizato K.;
Expression of the helix-loop-helix type negative regulators of
differentiation during limb regeneration in urodele and anuran.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB019514; BRA76631.1;
PiterPro; IRR001092; HLH_basic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 31.1%; Score 51; DB 13; Length 141;
1. Similarity 46.2%; Pred. No. 10;
12; Conservative 2; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16; Length 408;
21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00353; HLH; 1.
PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
SEQUENCE 141 AA; 15443 MW; C2012A212585C4A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam: PF00149; Metallophos; 1.
TIGRRAMs; TICR00619; sbcd; 1.
Exonuclease; Complete proteome.
SEQUENCE 408 AA: 46682 MW; CAEE3E17CFAE2B39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 AA.
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92 VAAGPLARDHGIIMVGTPKS 111
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                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Schulter U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
Nyakatura G., Mewes H.W., Mannhaupt G.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                           QBWZT3;

Q1-MAR-2002 (TTEMBLrel. 20, Last sequence update)

O1-MAR-2002 (TTEMBLrel. 20, Last sequence update)

O1-MAR-2002 (TTEMBLrel. 20, Last annotation update)

Hypothetical 21.3 kDa protein.

BBL21.040.

Burorspora crassa.

Buraryota: Fungi: Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
31.1%; Score 51; DB 3; Length 187;
Best Local Similarity 55.6%; Pred. No. 13;
Matches 10; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
German Neurospora genome project;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL669989; Cap21090.1; -.
Hypotherical protein.
SEQUENCE 187 AA; 21262 MW; 235332C807CC9F24 CRC64;
                                                                                                              187 A.A.
                  3 DSHLGAGPAAACHGHLLLGNPKNSAS 28
                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IKDSHLGAGPAAACHGHL 18
                                                                                                              PRELIMINARY;
                                                                                                              Q8WZT3
                                                                              RESULT 15
Q8WZT3
                                                                                                              õ
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Search completed: June 3, 2003, 19:23:56 Job time : 9.42683 secs

49 IGTSHLDSSPAAAHGDM 66

6 G

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 3, 2003, 19:18:46; Search time 1.76423 Seconds (without alignments) 728.798 Million cell updates/sec Run on:

Title: Perfect score:

US-09-938-703-6_COPY_185_215 164 1 INDSHLGAGPAAACHGHLLIGNPRNSASVSK 31 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 160% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	009675 schizosacch	Q9rqb4 helicobacte		Q9pbg5 xylella fas				_	_	Q9eq60 rattus norv	P16084 butyrivibri	P52711 hordeum vul	O15084 homo sapien	P52218 paracoccus		P07769 acinetobact	Q9w552 drosophila	075069 homo sapien	088942 mus musculu			P33485 pseudorable		_	Q12018 saccharomyc	Q03600 caenorhabdi	Q8z540 salmonella	052325 salmonella	083571 treponema p	Q01551 burkholderi	P51957 homo sapien		P20135 gallus gall
ID	YA02_SCHPO	HMCT_HELFE	V70K_OYMV	NADD_XYLFA	INC1_ECOLI	IF2P_AERPE	YFBG_ECO57	YFBG_ECOLI	FA8_MOUSE	CCAH_RAT	BGLS_BUTFI	CP23_HORVU	X379_HUMAN	CCMA_PARDE	THIE_PASMU	BENA_ACICA	VP26_DROME	Y481_HUMAN	NFC1_MOUSE	QA1F_NEUCR	HDA9_HUMAN	VNUA_PRVKA	FA8_HUMAN	HMEV_DROME	CC53_YEAST	INA1_CAEEL	YFBG_SALTI	YFBG_SALTY	TKT_TREPA	TBUD_BURPI	NEK4_HUMAN	RM32_HUMAN	GTT1_CHICK
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% Query Match	34.1	31.4	30.2	29.6	29.3	29.3	29.0	29.0	29.0	29.0	28.7	28.4	28.4	28.0	28.0	28.0	28.0	28.0	27.7	27.7	27.7	27.7	27.7	27.4	27.4	27.4	27.1	27.1	27.1	27.1	27.1	26.8	26.8
Score	56	51.5	49.5	48.5	48	48	47.5	47.5	47.5	47.5	47	46.5	46.5	46	46	46	46	46	45.5	45.5	45.5	45.5	45.5	45	45	45	44.5	44.5	44.5	44.5	44.5	44	44
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P43352 mus musculu P1124 bacteriopha P11124 bacteriopha P73867 synechocyst O9P145 chlamydia m P4429 haemophilus P2958 actinophane (01846 saccharomyc P57212 buchnera ap (1092 strizoacch P41247 homo sapien P29417 penicillium
RA52_MOUSE VP2_BPPH6 ATKB_SYNY3 PRFG_CHLMU YBGK_HAEIN AAC_ACTUT MOMI_YEAST RISA_BUCAI RAOD_SCHPO GS2_HUMAN RRPP_SYNV XRNA_PENCH
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ALIGNMENTS

				Ş					Lyne R., Stewart A.,	Peat N., Hayles J., Baker S., Basham D., Bowman S.,	all T., Fraser A.,	S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,	idiic a., dayeta h., I S., McLean J.,	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,	Sharp S.,	Stevens K.,	monprez B.,	Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Cabel C. Euchs W. Pritze C. Wolzer P. Moestl D. Wilhert H.	ach H., Reinhardt R., Pohl T.M.,	B., Wambutt R., Purnelle B., S. Glouy S. Lelaure V. Mottier S	Hunt C., Moore K., Hurst S.M.,	Garzon A., Thode G.,	Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,	Potashkin J.,	•	280W (YEAST).			Tt is produced through a collaborat	and the EMBL outstation	the Buropean Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no	is not removed. Usage by and for commercian not removed. Usage by and for commercian or served to the commercial served t		1117
		_	н	Schizosaccharomyces pombe (Fission yeast). Eukarvota: Fungi: Ascomvoota: Schizosaccharomycetes	Schizosaccharomycetales; Schizosaccharomycetaceae;				M., L	[., Peat N., Hayles J., Baker S., Basham D., Brown D. Brown S. Chillingsorth T. Chir	Feltwe	Hidal	Donale	Nible Pabl	r K.,	S	GF.	fer M	einha	., Pu:	oore)	Lucas M., Rochet M., Gaillardin C., Tallada V.A., Daga B.B. Crisado I. Timenes I. Sanches M. del	trong	т. Тяр Р	The genome sequence of Schizosaccharomyces pombe.";	ITE 415:8/I-88U(2002), SIMILARITY: RELONGS TO THE YMR322C/YOR391C/YPE,280W	OMBE		a di libo	CS al	e are	Usag		! !
;	AA.	te) date	some). haroi	yceta				yne]	, Ba		9	M K	. A	eege	ares	en J	chae Mo		t E	, X	ada e ² M	Arms	lsen Ni	ces	OR39	(S.P		70.0	mati	Ther g	ed.	}	! ! !
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	PRT;	sequence update) annotation update)	.02c ir	lasic	Lzos			2936/	ream		A .	Z,	, Le	×, c	unde:	ares	y a. ert	Rieg	1 A 1 : :	er H	z	din .	Morri	ie W Barr	zosa	HE Y	SPAC	OLI	oria	tute of Bioi	Inst	is n	isb-	!
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1	SI (Rel	(Rel.	protein	Schizosaccharomyces pombe (Fission yeast) Eukarvota: Fungi: Ascomycota: Schizosacch	omy	SCRIZOSACCHAIOMYCES. NCBI_TaxID=4896;	[1] SEQUENCE FROM N.A.	STRAIN=972; MFDLINE=21848401: D:::bMed=11859360:	llian	Peat	Conne	3oble	nes]	oule		Simme	Woodward J., Volckaert G	Van	ange	nerma	Galibert F., Aves S.J., Xiang	chet	, Re	LOW V	seda	P - T /	06/SI	SIMILARITY: SOME, TO E.COLI YEDU.	This SWISS-DROT entry is	Swi	Bio.	modified and this	or send an email)
			cal 02C.	char	char	D-48	FRO	2;	Gwi]		3 ° ` .:		, E	ΣC	. ₩	"		۲, ن ورز	Ä	Zim		ğ ć	, A	i.c	e la	L3:6.	F7.	ARI	d-8	the	non	and	. E	:
	SCHP 5; V-19	V-19 N-20	heti H10.	osac	osac	Taxi	NCE	N=97	, ;	SO:	ns N	es	, <u>, , , , , , , , , , , , , , , , , , </u>	7.7	rfor	on i	ard.	ens) ¥	P.,	ert	χ, α Σ, α	guez	itti ovs)	genc	e 4J	PAC	IMI	SWI	e d	surog by	ied	pue	
T 1 SCHPO	YA02_SCHPO Q09675; Q1-NOV-1995	01-NOV-1995 15-JUN-2002	Hypothetical SPAC5H10.02C	chiz	chiz	NCBI_TaxID=4896;	1.] EQUE	STRAIN=972;	pool	Sgouros J., E	Collins M.,	Gentles	ames	loone 1 tre	uthe	kelt	ay to	Peltj Sabel	Orzy	ger	alit	ucas	Odir	erru	The	atur i - i			2	between	the F	nodi1	or se	
SU 02																					_) r)		-				_	
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                                                                                                                                                                                                                                                                                                                                                                                                                "Membrane topology of Cada homologous P-type ATPase of Helicobacter pylori as determined by expression of phoA fusions in Escherichia coli and the positive inside rule."; Res. Microbiol. 150:507-520(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: COUPLES THE HYDROLÝSIS OF ATP WITH THE TRANSPORT OF CADMIUM, ZINC AND COBALT OUT OF THE CELL (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + H(2)O + Cd(2+)(ID) = ADP + phosphate +
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cd(2+)(out)
CaralxTIC ACTIVITY: ATP + H(2)0 + Zn(2+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfan: PF00702; Hydrolase; 1.

PRINTS: PR0019: CATATPASE.

PRINTS: PR00941: CDATPASE.

PROSITE: PS00164; APPASE_EL_E2; FALSE_NEG.

PROSITE: PS00147; HWA_1; FALSE_NEG.

PROSITE: PS0846; HWA_2; 1.

Hydrolase: Transmembrane; Phosphorylation; Magnesium; ATP-binding; Metal-binding; Cadmium; Zinc; Cobalt.

DOMAIN 1 72 CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20043416; PubMed-10577484;
Melchers K., Schuhmacher A., Buhmann A., Weitzenegger T., Belin D.,
Grau S., Ehrmann M.;
                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULA LOCATION: Integral membrane protein.
-!- SINITARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
(E1-E2 APPASES). SUBFAMILY IB.
-!- SIMILARITY: CONTAINS 1 HMA DOMAIN.
                                                                                                   6;
                                                                          Length 240;
                                                                                                                                                                                                                                   COCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Co-UNN-2002 (Rel. 41, Last annotation update)
(EC 3.6.3.5).
                                                                                                   6; Indels
EMBL; Z49811; CAA89952.1; -.
InterPro; IRR002818; ThiJ.
Fam; PF01965; ThiJ; 1.
Hypotherical protein.
SEQUENCE 240 AA; 26116 MW; 22C5614F06D56296 CRC64;
                                                                          Score 56; DB 1;
Pred. No. 0.52;
                                                                                                                                                                                                              681 AA.
                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF125316; AAF12735.1; -.
InterPro; IPR001757; ATPase_E1-E2.
InterPro; IPR001365; Cad_ATPase.
InterPro; IPR001934; HeavyMe_transpt.
InterPro; IPR001454; Hlgnase/hydrlase.
Pfam; PF00122; E1-E2_ATPASE; 1.
                                                                                                                                                                                                               PRT;
                                                                                                                                       11 AAACHGHLLLGNPKNSASV 29
                                                                          34.18;
57.98;
                                                                                                 Conservative
                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                              Helicobacter felis.
                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zn(2+)(Out)
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Best Local S
Matches 11
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ononis yellow mosaic virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Tymovirus.
NCBL_TaxID-12153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -! FUNCTION: NOT KNOWN.
-!- SIMILARITY: TO 65 TO 70 KDA PROTEIN FROM OTHER TYMOVIRUSES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
              EXTRACELLUIAR (BY SIMILARITY).
2 (BY SIMILARITY).
2 (CYTOPLASMIC (BY SIMILARITY).
3 (BY SIMILARITY).
4 (BY SIMILARITY).
4 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 597;
                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 681;
                                                                                                                                                                                                      CYTOPLASMIC (BY SIMILARITY).
7 (BY SIMILARITY).
EXTRACELLUIAR (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                  5 (BY SIMILARITY).
EXTRACELLULAR (BY SIMILARITY).
6 (BY SIMILARITY).
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MAGNESIUM (BY SIMILARITY).
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InterPro; IPR004935; Tymo_45_70kDa.
Pfam; PF03251; Tymo_45kd_70kd; 1.
SEQUENCE 597 AA; 65985 MW; 8A0BE4C2A7D329F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      913834388D4FBC5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 30.2%; Score 49.5; DB 1;
Best Local Similarity 37.5%; Pred. No. 12;
Matches 12; Conservative 4; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    597 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.4%; Score 51.5; E 52.6%; Pred. No. 6.7; tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                              POTENTIAL
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SEQUENCE FROM N.A.
MEDLINE-90021186; PubMed=2800337;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 GAGPAAACHGHLLL-GNPK 24
                                                                                                                                                                                                                                                                                                                                                                                                                      73747 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J04375; AAA46795.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similaricy
hes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                      681 AA;
388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 kDa protein.
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P20130;
                  DOMAIN
TRANSMEM
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IF2P_AERPE
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IF2P_AERPE
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RA Alvarenga R. Alves L.M.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R.A., Reinach F.C., Arruda P., Baia G.S., Baptista C.S., Barros M.H., Bonaccorsi E.D., Bordin S., Bowe J.M., Briones M.R.S., Bueno M.R.P., Camargo L.E.A., Carraro D.M., Carrer H., R. Bueno M.R.P., Camargo L.E.A., Carraro D.M., Carrer H., R. Coltutho L.L., Cristofani M., Dias Meto E., Docena C., El-Dorry H., R. Fraga J.S., Franco S.C., Franco M.C., Frohme M., Furlan L.R., Goutinho L.L., Cristofani M., Dias Meto E., Docena C., El-Dorry H., R. Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., Gondman G.H., Goldman M.H.S., Gomes S.L., Kitajima J.P., R. Hodeisel J.D., Junqueria M.L., Kemper E.L., Kitajima J.P., R. Miraca E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A., Martins E.M.E., Martins E.M.F., Martins C.L., Martins E.M.F., Martins C.L., Martins E.M.F., Martins C.L., Androdo M.A., Mactalia R.M., Mascimento A.L., Matto L.E.S., Monon D.H., Wobrega F.G., Nunes L.R., Oliveira M.A., Rachado M.A., Mascimento A.L.T.O., Netto L.E.S., A de Oliveira M.C., de Oliveira M.C., Pesquero J.B., Roberto P.G., Rodrieus W.J., Pesquero J.B., Roberto P.G., Rodrieus W.J., Pesquero J.B., Roberto P.G., Rodrieus W.J., Cavasaski H.E., A de Souza A.D., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., Vallada H., Van Sluye M.A., Varlovski-Almeida S., Vettore A.L., Allada H., Van Sluye M.A., Varlovski-Almeida S., Vettore A.L., Thrustra M.C., Bandenson P.C., Stubal J.C., Stubal J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: CATANYZES THE REVERSIBLE ADENYLATION OF NICOTINATE MONONUCLEOTIDE (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + nicotinate ribonucleotide = diphosphate
                                                                                                                        15-JUV (Rel. 40, Last sequence update)
15-JUV 2002 (Rel. 41, Last annotation update)
Probable nicotinate-nucleotide adenlylitransferase (EC 2.7.7.18)
(Deamido-NBD(+) pyrophosphorylase) (Deamido-NBD(+) diphosphorylase)
(Nicotinate mononucleotide adenlylitransferase) (NAMN
NADD OP POTITE
                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRFAMS; TIGR00125; cyt_tran_rel; 1. TIGRFAMS; TIGR00482; TIGR00482; TIGR00482; TIGR00482; TIGR00482; TIGR00482; Nucleocidylitransferase; Nucleocidylitransferase; Nucleocidylitransferase; Nab; Complete proteome. SEQUENCE 222 AA; 24497 MM; ASBG3BAASESA90589 CRC64;
553 SHLPSSPSSACSGDSFASCSSFGPSNPTSSAS 584
                                                                                              222 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE NADD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR004821; Cyt_tran_rel.
InterPro; IPR005248; NAMN_adtrnsfrase.
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20365717; PubMed-10910347;
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                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                            fastidiosa.
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                         NADD OR XF2179
                                                                                                NADD_XYLFA
                                                                                                                                                                                                                                                                                              Kylella
                                                                                                                                                                                                                                                                                                                                     (vlella
                                                                             NADD_XYLFA
                                                         RESULT 4
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MEDLINE-952914646; PubMed-7773415;

MEDLINE-952914646; PubMed-7773415;

Thomas C.M., Smith C.A., Ibbotson J.P., Johnston L., Wang N.;

"Evolution of the kora-oriV segment of promiscuous IncP plasmids.";

Microblotogy 141.1201-1221(1995).

-I FUNCTION: THIS IS ONE OF THE PROFERINS ENCODED BY THE TREB OPERON;
IT IS INVOLVED IN PLASMID MAINTENANCE AND REPLICATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macartney D.P., Williams D.R., Stafford T., Foster A., Thomas C.M. "Evolution of the partitioning and global regulation functions of the trans control region.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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               1; Length 222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the IncP central control region.";
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 358 AA; 38246 MW; 44859F07844167EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                      5,
                                                                                                                                                                                                                                                                                                                                     INC1_ECOLI STANDARD; PRT; 358 AA. 052312; 05283; P71175; 0510-10V-1997 (Rel. 35, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Probable translation initiation factor IF-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          617 AA.
            Score 48.5; DB:
Pred. No. 6.2;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -! - SIMILARITY: BELONGS TO THE PARA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000707; ATPase_ParA. Pfam; PF00991; ParA; 1.
                                                                                                                                                                                        170 HGHLWLLNOPPNPSSASK 187
                                                                                                                                15 HGHL-LLGNPKNSASVSK 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-109 FROM N.A.
Query Match
Best Local Similarity 61.19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid IncP-beta R751.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli.
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SEQUENCE FROM N.A.
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YFBG_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                        MEDLINE-99310339; PubMed-10382966;

A MEDLINE-99310339; PubMed-10382966;

A Gawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,

A Jin no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,

A Hosoyama A., Fukui S., Magai Y., Mishijima K., Makazawa H.,

A Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,

A Manazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,

A Nakamura Y., Nomura N., Sako Y., Kikuchi H.;

"Complete genome sequence of an aerobic hyper-thermophilic remarchaeon, Aeropyrum pernix Kl.";

EL DNA Res. 6:83-101(1999).

"THE BININI GO F THE FORMILARTIONINIA-TRNA TO RIBOSOMES. SEEMS TO FUNCTION ALONG WITH EIF-2 (BY SIMILARTY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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15-UNN-2002 (Rel. 41, Last sequence update)
15-UNN-2002 (Rel. 41, Last sequence update)
Hypotherical protein yfbG.
YFBG OR 23513 OR ECS3143.
Seofberichia coll 0157:H7.
Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaces; Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n 29.3%; Score 48; DB 1; Length 617; Similarity 27.6%; Pred. No. 20; 8; Conservative 8; Mismatches 13; Indels
                            Aeropyrum pernix.
Aeropyrum pernix.
Aerobae, Cremarchaeota; Thermoprotei; Desulfurococcales;
Desulfurococcaceae; Aeropyrum.
NCBL_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 GTP (BY SIMILARITY).
91 GTP (BY SIMILARITY).
144 GTP (BY SIMILARITY).
68520 MW; 493DC149C6028EB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01176; IF2; FALSE_NEG.
Initiation factor; Protein biosynthesis; GTP-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR005225; Small_GTP.
Interpro; IPR005444; TFF.aIF-2.
Pfam, PF03144; GTP_EFUT; 1.
Pfam, PF03144; GTP_EFUT; 1.
THRTS; PR00315; ELCNORATNECT.
TIGREAMS; TIGRD0231; Small_GTP; 1.
TIGREAMS; TIGR00491; aIF-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AP000064; BAA81387.1; -.
InterPro; IPR004161; EFTU_D2.
InterPro; IPR000795; EF_GTPbind.
InterPro; IPR000178; IF2.
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617 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-0157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed-11286796;
MEDLINE-21156231; PubMed-11286796;
MEDLINE-21156231; PubMed-11286796;
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterchemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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STRAIN-KIZ, VMG16555,
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                      Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfal G., Hackett J., Klink S., Boutin A., Shoo Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.,
Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
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EMBL, AP005561; BAB35566.1; -.
InterPro: IPR002376; formyl_transf.
InterPro; IPR004187; Formyl_transf.
Pfam, PP00551; formyl_transf; 1.
Pfam; PP00551; formyl_transf; 1.
Hypothetical protein; Transferase; Methyltransferase;
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15-UUL-1999 (Rel. 38, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein yfbG.
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42.1%; Pred. No. 25;
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STRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed-11206551;
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SULFATION (REQUIRED FOR WWF BINDING)
(BY SIMILARITY).
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PROSITE; PS01286; FA58C_2; 2.
Blood coagulation; Repeat; Plasma; Acute phase; Calcium; Signal; Glycoprotein; Sulfation.

Signal: 110
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PLASTOCYANIN-LIKE 2.
F5/8 TYPE A 2.
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PLASTOCYANIN-LIKE 6.
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              -!- SIMILARITY: CONTAINS 2 F5/8 IYPE C DOMAINS.
-!- SIMILARITY: STRONG, TO COAGULATION FACTOR V.
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InterPro; IPR0001117; Cu-oxidase.
InterPro; IPR0001117; Cu-oxidase.
Pfam; PF00394; Cu-oxidase; 2.
Ffam; PF00754; F5_F8_Lype_C; 2.
SMARY; SMO0731; FASEC; 2.
PROSITE; PS00079; MULTCOPPER_OXIDASE1; 3.
PROSITE; PS01285; FASEC_1; 2.
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2 PLASTOCYANIN-LIKE REPEATS.
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                                                                                                                                                                                  "Construction of a contiguous 874-kb sequence of the Escherichia coli - K12 genome corresponding to 50.0-68.8 min on the linkage map and analysis of its sequence features.";

DNA Res. 4:91-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomics 16:374-379(1993).

--- FUNCTION: FACTOR VIII, ALONG WITH CALCIUM AND PHOSPHOLIPID, ACTS
AS A COPACTOR FOR FACTOR IXA WHEN IT CONVERTS FACTOR X TO THE
ACTIVATED FORM, FACTOR XA.

--- SUBCELLOIAR LOCATION: Extracellular.

---- SUBCELLOIAR LOCATION: Extracellular.

---- SIMILARITY: CONTAINS 3 F5/8 TYPE A DOMAINS; EACH IS COMPOSED OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                              Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K., Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N., Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H., Oghima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S., Tagami H., Takahashi H., Takeda J., Takemoto K., Uchara K., Wada C., Yamagata S., Horluchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Tast sequence update)
11-JUN-2002 (Rel. 41, Last annotation update)
Coagulation factor VIII precursor (Procoagulant component).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 660 AA; 74288 MW; A430928AB4041FA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Transferase; Methyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-C57BL/6 X CBA; TISSUE-Liver;
MEDILNE-9330051; PubMed-831457;
Elder B. Lakich D., Gitschier J.;
"Sequence of the murine factor VIII cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.0%; Score 47.5; I Local Similarity 42.1%; Pred. No. 25; es 8; Conservative 6; Mismatches
                                                                                                                                                                                                                                                             -! - SIMILARITY: BELONGS TO THE FMT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ecclency Education (1976).

Ecclency EPRO04187; Formyl trans_C. InterPro: IPR004187; Formyl_transf. Pfam; PP00551; formyl_transf. Pfam; PP00511; formyl_transf; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              558 CDGEIINIGNPENEASIEE 576
                                                                       MEDLINE-97349980; PubMed-9205837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 CHGHLL-LGNPKNSASVSK 31
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000315; AAC75315.1; -.
EMBL; D90856; BAA16078.1; -.
EMBL; D90857; BAA16082.1; -.
HSSP; P23882; 1FMT.
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Mouse).
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SEQUENCE FROM N.A.
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                                    SEQUENCE FROM N.A.
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Mus musculus (Mou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAB_MOUSE
Q06194;
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                                                                                                                                                                                                                  Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
Calcium channel; Glycoprotein; Repeat; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S4 OF REPEAT II (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S5 OF REPEAT II (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S1 OF REPEAT II (POTENTIAL).
S2 OF REPEAT III (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S3 OF REPEAT III (POTENTIAL).
S3 OF REPEAT III (POTENTIAL).
S4 OF REPEAT III (POTENTIAL).
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SE OR REBEAT III (POTENTIAL).
SE OR REBEAT III (POTENTIAL).
STOPLASHIC (POTENTIAL).
SI OF REPEAT IV (POTENTIAL).
SZ OF REPEAT IV (POTENTIAL).
SZ OR REPEAT IV (POTENTIAL).
SZ OF REPEAT IV (POTENTIAL).
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CYTOPLASHIC (POTENTIAL).
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SS OF REPEAT I (POTENTIAL).
STOPLASHIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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S6 OF REPEAT IV (POTENTIAL)
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S1 OF REPEAT I (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S2 OF REPEAT I (POTENTIAL).
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S3 OF REPEAT I (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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POLY-HIS.
POLY-ARG.
                                                                   EMBL; AF290213; AAG35187.1; -.
InterPro; IPR001682; Ca/Na_pore.
InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR002077; Ca_channel.
InterPro; IPR000836; M+channel_nlg.
InterPro; IPR000836; PKD_2.
                                                                                                                                                                                                     PRINTS; PR01629; TVDCCALPHA1.
                                                                                                                                                        Pfam; PF00520; ion_trans; 4.
PRINTS; PR0167; CACHANNEL.
PRINTS; PR01433; POLYCISTIN2.
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   RT T-TYPE CALCIUM CHANNELS.";

T-TYPE CALCIUM CHANNEL ALCOURT CHANNELS.";

T-TYPE CALCIUM CHANNELS CHANNEL ALPHA-I SUBNITS.";

T-TYPE CALCIUM CHANNELS TO THE CALCIUM CHANNEL ALPHA-I SUBNITS.";

T-TYPE CALCIUM CHANNELS TO THE CALCIUM CHANNEL ALPHA-I SUBNITS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Voltage-dependent T-type calcium channel alpha-1H subunit (Cav3.1c).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCRORY J.E., Santi C.M., Hamming K.S.C., Mezeyova J., Sutton K.G., Baillie D.L., Stea A., Snutch T.P.,
"Molecular and functional characterization of a family of rat brain
                                                                                                   (POTENTIAL)
                                                                                                                                                                                                     Э,
                                                                         (POTENTIAL)
                                                                                     (POTENTIAL)
                                 (POTENTIAL)
                                              (POTENTIAL)
                                                          (POTENTIAL)
                                                                                                                                 POTENTIAL)
                                                                                                                                                                          DB 1; Length 2319;
                                                                                                                                                                                                     Indels
                                                                                                                                           CRC64;
                              (GLCNAC. . .)
(GLCNAC. . .)
(GLCNAC. . .)
                                                                      (GLCNAC. . .)
                                                                                                                  (GLCNAC. . .)
                                                                                                 (GLCNAC. . .)
                                                                                                                                           MW; FD054DE051DB2A01
                                                                                                                                                                                                     12:
                  GLCNAC
                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                2 KDSHLG-AGPAAACHGHLLLGNPKNSASVS 30
                                                                                                                                                                                      88;
                                                                                                                                                                        Score 47.5;
Pred. No. 88
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MEDLINE=21264893; PubMed=11073957;
                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                       29.0%;
40.0%;
                                                                                                                                             266148
                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat)
 1255
1268
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1274
1302
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1340
1378
                                                                                                                                                                                      Similarity
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                                                          CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBUNIT: CARBOXYPEPTIDASE II IS A DIMER, WHERE EACH MONOMER IS COMPOSED OF TWO CHAINS LINKED BY A DISULEIDE BOND (BY SIMILARITY).
-i- DBYELOPMENTAL STAGE: EXPRESSED IN THE GERMINATING EMERYO. ALSO FOUND IN THE ROOTS AND SHOOTS OF THE GROWING SEBDLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The expression of serine carboxypeptidases during maturation and germination of the barley grain.";

proc. Natl. Acad. Sci. U.S.A. 91:8209-8213(1994)

-- CATALVITC ACTIVITY: Preferential release of a C-terminal arginine or lysine residue.
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
SERINE CARBOXYPEPTIDASE II-3, CHAIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LINKER PEPTIDE (BY SIMILARITY).
SERINE CARBOXYPEPTIDASE II-3, CHAIN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- PTM: THE LINKER PEPTIDE IS ENDOPROTECLYTICALLY EXCISED DURING ENZYME MATURATION (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY $10.
                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine carboxypeptidase II-3 precursor (EC 3.4.16.6) (CP-MII.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
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N-LINKED GLCNAC. .) (POTENTIAL)
N-LINKED GLCNAC. .) (POTENTIAL)
N-LINKED GLCNAC. .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-CV. Alexis; IISSUE-Grain;
MEDLINE-94336715; Pubmed-7520177;
Dal Degan F., Rocher A., Cameron Wills V., von Wettstein D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein; Zymogen; Signal;
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BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
    Indels
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BY SIMILARITY.
    4; Mismatches
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Interpro: IPR0101563; Ser_ine_carbpept.
Pfam, PR00456; Serline_carbpept; 1.
PRINTS; PR00724; CRBOXYPTASC.
Prodom; PD001189; Serline_carbpept; 1.
PR05ITE; PS00131; CARBOXYPEPT_SER_SER; 1.
PR05ITE; PS00560; CARBOXYPEPT_SER_HIS; 1.
                                        5 HLGAGPAAACHGHLLLGNPKNSASVSK 31
                                                                              28 HIELSCEAACEGMVLLKNDRNVLPIRK 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase, Carboxypeptidase,
Multigene family.
SIGNAL 1 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X78877; CAA55478.1; -. HSSP; P08819; 1WHT.
                                                                                                                                                                                                                                                                                                                         Hordeum vulgare (Barley).
  Conservative
                                                                                                                                                                                   STANDARD:
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CARBOHYD
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  Matches
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                                                                          CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
SELECTIVITY AND PERMEABILITY
                                      CALCIUM ION SELECTIVITY AND PERMEABILITY
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1990 (Rel. 14, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
Beta-glucosidase A (E. 3.2.1.21) (Gentiobiase) (Cellobiase) (Beta-D-glucoside glucohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae;
                                                                                                                                                          192 192 N-LINKED (GLCNAC. . ) (POTENTIAL).
271 271 N-LINKED (GLCNAC. . ) (POTENTIAL).
147 N-LINKED (GLCNAC. . ) (POTENTIAL).
2359 AA: 261138 MW; F738083E94180081 CRC64;
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                                                                                                                                                                                                                                                                Score 47.5; DB 1; Length 2359;
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Pred. No. 38;
                                                                                                                                                                                                                                                                                                      5; Indels
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1DBF578DCA18B6F3 CRC64;
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Pfam: PP01915; GlyCo_hydro_3 C; 1.
PRINTS; PR01913; GLHYDRLARE3.
PROSITE; PS00775; GLYCOST_HYDROL_F3; 1.
Hydrolase; Glycosidase; Cellulose degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        830 AA.
                                                             SIMILARITY)
                   SIMILARITY
                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                   89;
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                                                                                                                                                                                                                                                                                 Pred. No.
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                                                         (BY
                                                                                                                                                                                                                                                                                                                                                                                637 GAGAPGAAVHSPLSLGSPR 655
                                                                                                                                                                                                                                                                                                                                            7 GAG-PAAACHGHLLLGNPK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
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                                                                                                                                                                                                                                                                29.08;
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InterPro; IPR001764; GH_3N.
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                                                                                                                                                                                                                                                              Query Match 29.0
Best Local Similarity 57.9
Matches 11; Conservative
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Best Local Similarity
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SEQUENCE FROM N.A.
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P16084;
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SEQUENCE
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                                   SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page D., Pearce D.A., Norris H.A., Ferguson S.J.;

"The Paracoccus denitrificans ccmA, B and C genes: cloning and sequencing, and analysis of the potential of their products to form a haem or apo-c-type cytoohrome transporter.";

Microbiology 143:563-576(1997).

-I- FUNCTION: REQUIRED FOR THE EXPORT OF HEME TO THE PERIPLASM FOR THE BIOGENESIS OF C-TYPE CYTOCHROMES (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: Inner membrane-associated (Potential).

-I- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytochrome c-type blogenesis; Transport; APP-binding; Inner membrane. NP_BIND 36 43 ATP (POTENTIAL). SEQUENCE 211 AA; 21978 MW; 3C40E54C1B37CEFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                      Gaps
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1-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Heme exporter protein A (Cytochrome c-type biogenesis ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Paracoccus denitrificans.
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
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                                                                                                                                                                                                                        DB 1; Length 1059;
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Pred. No. 14;
3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                 8; Indels
                                                                                                                                                                              C1F55E6CFE494770 CRC64;
                                                                                                                                                                                                                                                                                                                                             617 VKDYILKRTPIHAAATNGHSECLRLLIGNAEPQNAVDI 654
                                                                                                                                                                                                                                                                                                           1 IKDSHLGAGP--AAACHGH-----LLLGN--PKNSASV 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 AA.
                                                                                                                                                                                                                                                                 6; Mismatches
                                                                                                                                                                                                                      Score 46.5; Pred. No. 57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00382; AAA; I.
TIGREAMS; TIGR01189; ccmA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z71971; CAA96502.1; -.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transportr.
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    ANK 20
ANK 21
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ANK 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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MEDLINE-97195802; PubMed-9043133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 SHLGAGPAACHGHLLLGNPK 24
                                                                                                                                                                              113465 MW;
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39.5%;
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                                                                                                                                                                                                                                                                 15; Conservative
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  720
753
790
8823
8857
8851
960
691 724 754 751 751 751 753 828 868 861 895 931 961 1059 AA;
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Best Local Similarity
Matches 15; Conserv
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Best Local Similarity
Matches 10; Conserv
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CCMA_PARDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nagase T., Ishikawa K.I., Nakajima D., Ohira M., Seki N.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"prediction of the coding sequences of unidentified human genes. VII.
The complete sequences of 100 new CDNA clones from brain which can
code for large proteins in vitro.";
DNA Res. 4:141-150(1997).

-: SIMILARITY: CONTAINS AT LEAST 27 ANK REPEATS.
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
  .) (POTENTIAL).
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                                                                DB 1; Length 516;
                                                                                                            Indels
N-LINKED (GLCNAC, ..) (P
D41AA1C56CF8D355 CRC64;
                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein KIAA0379 (Fragment).
                                                                                                                                                                                 11 IGAGPAAAAKARRTRQGDYLNRLRGSPSSRAS 50
                                                                                                                                                       6 LGAGPAAACHG-----HLLLGNPKNSAS 28
                                                              Score 46.5; DB Pred. No. 28; 3; Mismatches
                                                                                                                                                                                                                                                                                                           PRT; 1059 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PSS0088; ANK_REPEAT; 24.
PROSITE; PSS0297; ANK_REP_REGION; 1.
Hypothetical protein; Repeat; ANK repeat.
NON_TER 75 ANK 1.
REPEAT 46 75 ANK 2.
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HSSP; P80144; 2MYO.
                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
                    55913 MW;
                                                           tch 28.4%;
al Similarity 40.6%;
13; Conservative 3
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Pfam; PF00023; ank; 28.
SMART; SM00248; ANK; 26.
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307
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472
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                    516 AA;
                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                      Y379_HUMAN
015084;
CARBOHYD
                       SEQUENCE
                                                              Query Match
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163 AHLGRGGAAVIATHIDLGLPE 183

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-!- FUNCTION: COMDEMESS 4-METHYL.5-(FERRA-HYDROXXETHYL)-THIAZOLE MONOPHOSPHATE (THZ.-P) AND 4-AMINO-5-HYDROXXETHYL PYRIAIDINE PYROPHOSPHATE (HMP-PF) TO FORM THIAMINE MONOPHOSPHATE (TMP) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
-!- CATALYTIC ACTIVITY: 2-methyl-4-amino-5-hydroxymethylpyrimidine diphosphate + 4-4-methyl-5-(2-phosphonoxyethyl)-thiazole = diphosphate + 4-thiamine monophosphate.
-!- PATHWAY: Thiamine biosynthesis.
-!- PATHWAY: Thiamine biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Thiamine-phosphate pyrophosphorylase (EC 2.5.1.3) (TMP
Pyrophosphorylase) (TMP-PPase) (Thiamine-phosphate synthase).
                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
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Pfam: PF02581; TMP_TENI; 1
TIGRFAMS; TIGR006093; this: 1.
TIGRAMS; TIGR006093; this: 1.
SEQUENCE blosynthesis; Transferase; Complete proteome.
SEQUENCE 221 AA; 23736 MW; 2207E7EE52134 CRC64;
                                       221 AA.
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                                         PRT;
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SEQUENCE FROM N.A.
STRAIN-PM70;
MEDLINE-21145866; PubMed-11248100;
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                                         STANDARD;
                                                                                                                                                                                                    Pasteurella multocida
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                                         THIE PASMU
RESULT 15
THIE_PASMU
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Search completed: June 3, 2003, 19:22:57 Job time: 2.70423 secs

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7: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

Published_Applications_AA:*

Database

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 22, Appl Sequence 5, Appli Sequence 62, Appli Sequence 62, Appli Sequence 1726, App Sequence 212, App Sequence 21, App Sequence 2, Appli Sequence 4, Appli Sequence 6, Appli Sequence 155, Appli Sequence 1655, Appli Sequence 1655, Appli Sequence 10, Appli Sequence 10, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli	MOKINES RECEPTOR : ENCODING SAID RECEPTOR (OO.
US-09-938-330-22 US-09-938-330-22 US-10-205-368-5 US-09-814-1122-62 US-109-925-300-1726 US-109-925-300-1726 US-09-925-300-1726 US-09-93-3941-4 US-09-973-961-4 US-09-973-961-4 US-09-973-961-4 US-09-973-064-4 US-09-973-063-4 US-09-973-063-4 US-09-973-063-4 US-09-973-063-4 US-09-973-063-4 US-09-973-063-4 US-09-972-038-4 US-09-972-038-4 US-09-972-038-4 US-09-972-038-4 US-09-972-038-4 US-09-972-038-4 US-09-972-038-4 US-09-972-038-4 US-09-972-038-4 US-09-973-965-4	D INACTIVE CC-CHE TC ACID MOLECULES TO ACID MOLE
23 1 1 1 1 2 4 2 4 2 4 2 4 2 4 2 4 2 4 2 4	ALIGI 38-719-13 38-719-13 38-719-13 38-719-13 38-719-13 APPLICANT: SAMSON, MICHEL APPLICANT: SAMSON, MICHEL PARMENITIES, MARC TILBERT, FREDERICK TILBERT, FREDERICK TILBERT, FREDERICK TILBERT, FREDERICK TILBERT, FREDERICK TILBERT, FREDERICK TILBERT, ENDERS: AND NOCLEIC NUMBER OF SEQUENCES: 17 CORRESSEE: RODDE, MATTENS, STREET: 620 Newport Center CITY: Newport Beach STREET: 620 Newport Center CITY: Newport Beach STREET: 620 Newport Center COUNTRY: U.S.A. ZIP: 92666 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS SOFTWARE: PALENTIN RELEASE CURRENT APPLICATION NUMBER: UNKNOWN) PRIOR APPLICATION NUMBER: GF FILING DATE: 24-Aug-2001 CILSSIFICATION NUMBER: GF FILING DATE: 27-JULY-200 ATTORNEY/AGENT INFORMATION: NAME: Altman, Daniel E REGISTRATION NUMBER: 34,115 REGISTRATION POR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: TYPE: amino acids TYPE: SEQUENCE CHARACTERISTICS: TYPE: SEQUENCE SEQ ID NO: 13: SEQUENCE DESCRIPTION: SEQ ID NO:
20 20 20 20 20 20 20 20 20 20	
<u> </u>	RESULT US-091 Seque

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TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
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                                                                                                                                                                                                                                                                                              ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
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                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach
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ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 164; DB 10;
Pred. No. 5.9e-17;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-aug-2001
CLASSIFICATION: GUNKOWN>
PRIOR APPLICATION OF STREET
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORREY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Althan, Daniel B
REGISTRATION NUMBER: 34,115
REPERBUCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 INDSHLGAGPAAACHGHLLLGNPKNSASVSK 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 164; D
Best Local Similarity 100.0%; Pred. No. 5.9
Matches 31; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09938719; Patent No. US20020106742A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FREDERICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 34 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Newport Beach
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COMPUTER READABLE FORM:
                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
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                                                                                                                                      Gaps
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: <union-content of the content of
                                                                      Length 34;
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                                                                                                                                   Indels
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ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                ch 100.0%; Score 164; DB 10; Similarity 100.0%; Pred. No. 5.9e-17; 31; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 5.9e-17;
tive 0; Mismatches 0;
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                                                                                                                                                                                                1 IKDSHLGAGPAAACHGHLLLGNPKNSASVSK 31
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REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
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Patent No. US2002010870A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
YAMBENTER, MARC
WASSART, GILBERT
LIBERT
LIBERT, FREDERICK
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/09939226
Patent No. US20020110805A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
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LENGTH: 34 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
                                                                                              Best Local Similarity
Matches 31; Conserv
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Matches 31; Conserv
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US-09-938-703-13
US-09-938-719-13
                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: <u >color</u>
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 164; DB 10; Length 215; Best Local Similarity 100.0%; Pred. No. 5e-16; Matches 31; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                    Length 215;
                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                               tch 100.0%; Score 164; DB 10; al Similarity 100.0%; Pred. No. 5e-16; 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 IKDSHLGAGPAAACHGHLLIGNPKNSASVSK 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: GDKHOWN>
INFORMATION FOR SEQ ID NO: 6:
                                                            NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: «Unknown>
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                      1 IKDSHLGAGPAAACHGHLLLGNPKNSASVSK 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
APPLICATION NUMBER: 09/626,939
                                                                                                                                                                                                    ; TOPOLOGY: Linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-938-719-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-939-226-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 09/626,939
                  FILING DATE: 27-JULY-2000 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09939226
Patent No. US20020110805A1
GENERAL INFORMATION:
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VASSART, GILBERT
LIBERT, FREDERICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 215 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SECUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-09-939-226-6
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Sequence 43034, Application US/09864761
PREACH IN US20020048763A1
GENERAL INFORMATION:
APPLICANT: Renk, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL ITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aconica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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COMPUTER: IBM PC compatible
OPBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSER: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 164; DB 10; 100.0%; Pred. No. 5e-16;
185 IKDSHLGAGPAAACHGHILLIGNPKNSASVSK 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Altman, Daniel E
REGISTATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: «UDKNOWD>
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IKDSHLGAGPAACHGHLLLGNPKNSASVSK 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION: <unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TYPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-938-703-6
                                                                                                                                                                                                                   APPLICANT: SAMSON, MICHEL PARMENTIER, MARC VASSART, GILBERT LIBERT
                                                                                                                                            Sequence 6, Application US/09938703; Patent No. US20020110870A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 215 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: CA
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1 IKDSHLGAGPAAACHGHLLLGNPKNSASVSK 31

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Sequence 2, Application US/09938330

Patent No. US20020115838A1

BERREAL INFORMATION:

APPLICANT: Walke, D. Wade

APPLICANT: Hilbun, Erin

APPLICANT: Scoville, John

APPLICANT: Friddle, Carl Johan

FRIDE REFERENCE: LEX-0237-USA

FRIDE REPERENCE: LEX-0237-USA

FRIDE RELING DATE: 2000-06-22

FRIOR PRICH APPLICATION NUMBER: US 60/227,104

FRIOR PRICH APPLICATION NUMBER: US 60/223,796

FRIOR PRICH SEQ ID NOS: 26

SOFTWARE: FastSEQ for Windows Version 4.0

FROM IN ASI
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APPLICANT: Scoville, John
APPLICANT: Friddle, Carl Johan
APPLICANT: Friddle, Carl Johan
APPLICANT: Hu, Yi
APPLICANT: Hu, Yi
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INTERFORMENCE: LEX-0237-USA
CURRENT APPLICATION NUMBER: US/09/938,330
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: US 60/227,104
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                                                                                                                                                                                                                                                                                                                                                                                                                                              29.3%; Score 48; DB 10; Length 297;
45.0%; Pred. No. 43;
tive 5; Mismatches 6; Indels
                  PRIOR APPLICATION NUMBER: US 60/227,104
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 SHLGAGPAAACHGHLLLGNP 23
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Pattent No. US2020115838A1
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 SHVVSGPAAASAGSMVVDTP 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 SHLGAGPAAACHGHLLLGNP 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 45.08
Matches 9; Conservative
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US-09-938-330-2
                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Patent No. US20020115838al
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Fidle, Carl Johan
APPLICANT: Fridle, Carl Johan
APPLICANT: Turner, C. Alexander Jr.
TILE OF INVENTION: NO. US20020115838Alel Human Proteases and Polynucleotides Encodin
FILE SEFERENCE: LEX. US30920315838Alel Human Proteases and Polynucleotides CURRENT APPLICATION NUMBER: US/09/938,330
CURRENT APPLICATION UNMBER: US/09/938,330
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INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.93
INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.92
INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.92
INFORMATION: EXPLANAN HIT: AI696698.1, EVALUE 7.00e-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 33.5%; Score 55; DB 10; Length 84; 1 Similarity 50.0%; Pred. No. 0.98; 12; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-03
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2001-01-30
PRIOR PRIOR PLING DATE: 2001-01-30
PRIOR 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: MAP TO AL096816.12 OTHER INFORMATION: EXPRESSED IN BONE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 DSHLGGGPAATA-----GGPRTS 65
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 12; Conserva
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Wed Jun 11 09:06:32 2003

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APPLICANT: DALLOW, LALL,
APPLICANT: Scoville, John
APPLICANT: Scoville, John
APPLICANT: Friddle, Carl Johan
APPLICANT: Friddle, Carl Johan
APPLICANT: Hu, YI
APPLICANT: Hu, YI
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: NO. 0S20020115838Alel Human Proteases and Polynucleotides Enco
FITLE REPRENENCE: LEX-0237-105A
CURRENT APPLICATION NUMBER: US 60/227, 104
FRIOR PRINCENTING DATE: 2000-08-22
FRIOR PRINCED TO NUMBER: US 60/233, 796
FRIOR PRINCED TO NUMBER: US 60/233, 796
FRIOR PRINCED TO NOS: 26
SOFTWARE: FRASEQ for Windows Version 4.0
SOFTWARE: PRASEQ for Windows Version 4.0
SENOID NO 10
LENGTH: 1219
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APPLICANT: Walke, D. Wade
APPLICANT: Wallbu, Erin
APPLICANT: Hilbu, Erin
APPLICANT: Friddle, Carl Johan
APPLICANT: Friddle, Carl Johan
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVERTION: NO. US20020115838Alel Human Proteases and Polynucleotides Enco
FILE REFERENCE: LEX-0237-USA
CURRENT APPLICATION NUMBER: US 60/227,104
PRIOR APPLICATION NUMBER: US 60/227,104
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: US 60/233,796
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0
                                                                                                                                                                                                                                                               Length 1216;
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                                                                                                                                                                                                                                                            Query Match 29.3%; Score 48; DB 10; Length 12: Best Local Similarity 45.0%; Pred. No. 2.2e+02; Matches 9; Conservative 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Indels
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                                                        NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 1216
     PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR FILING DATE: 2000-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/09938330; Patent No. US20020115838A1; GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Hilbun, Erin
                                                                                                                                                                                                                                                                                                                                                                                                  54 SHVVSGPAAASAGSMVVDTP 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 SHLGAGPAAACHGHLLLGNP 23
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SHVVSGPAAASAGSMVDTP 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 8, Application US/09938330
; Patent No. US20020115838A1
                                                                                                                                                                                                                                                                                                                                                                     4 SHLGAGPAAACHGHLLLGNP 23
                                                                                                                                                         TYPE: PRT
; ORGANISM: homo sapiens
US-09-938-330-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: homo sapiens
US-09-938-330-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-09-938-330-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hilbun, Erin
APPLICANT: Fiddle, Carl John
APPLICANT: Friddle, Carl John
APPLICANT: Friddle, Carl John
APPLICANT: H. Yi
APPLICANT: H. Yi
APPLICANT: H. Yi
APPLICANT: H. Yi
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: NO. US20020115838Alel Human Proteases and Polynucleotides Encodin
FILE REPERENCE: LEX-C237-USA
CURRENT APPLICATION NUMBER: US 60/227,104
PRIOR APPLICATION NUMBER: US 60/227,104
PRIOR APPLICATION NUMBER: US 60/227,104
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 26
SOUTHARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Walke, D. Wade
APPLICANT: Wilbun, Erin
APPLICANT: Friddle, Carl Johan
APPLICANT: Friddle, Carl Johan
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US2000115838Alel Human Proteases and Polynucleotides Encodin
FILE REFERENCE: LEX-0237-USA
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                                                                                                                                                                                                                                                                                    29.3%; Score 48; DB 10; Length 486; ilarity 45.0%; Pred. No. 77; Conservative 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 2.2e+02;
5; Mismatches 6; Indels
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/09938330 Patent No. US20020115838A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
                                                                                                                                                                                 ; TYPE: PRT; ORGANISM: homo sapiens
US-09-938-330-6
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CRGANISM: homo sapiens
US-09-938-330-14
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-10-205-368-4

J Gequence 4, Application US/10205368

Publication No. US20030092621A1

GENERAL INFORMATION:
APPLICANT: RACSTING, MICHAEL J.
APPLICANT: RACSTING, MICHAEL J.
TILLE REPRENCE: 08702.0094-00000

CURRENT FILE REPRENCE: 08702.0094-00000

CURRENT FILING DATE: 2002-07-26

PRIOR FILING DATE: 2002-07-26

PRIOR APPLICATION NUMBER: 60/308,386

PRIOR APPLICATION NUMBER: 60/308,386

PRIOR PRILING DATE: 2001-08-29

NUMBER OF SEQ ID NOS: 21

SEQ ID NO 4

LENGTH: 1223

LENGTH: 123

TYPE: PRT

VERALL HOMO SADIENS

US-10-205-368-4
; PRIOR FILING DATE: 2000-09-19; NUMBER OF SEQ ID NOS: 26; SOFTWARE: PastSEQ for Windows Version 4.0; SEQ ID NO 8; LENGTH: 12.2; TYPE: PRT ORGANISM: homo sapiens US-09-938-330-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: June 3, 2003, 19:36:00 Job time : 8.43496 secs
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54 SHVVSGPAAASAGSMVVDTP 73
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54 SHVVSGPAAASAGSMVVDTP 73
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GenCore version 5.1.6
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OM protein - protein search, using sw model

June 3, 2003, 19:20:46; Search time 3.40244 Seconds Run on:

(without alignments)
875.891 Million cell updates/sec

US-09-938-703-6_COPY_185_215

164 1 IKDSHLGAGPAAACHGHLLLGNPKNSASVSK 31 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	hypothetical prote	4		hypothetical prote	DNA repair exonucl	hypothetical 66K p	probable mitochond	conserved hypothet	cytochrome P450 2D	hypothetical prote	inclusion membrane	probable translati	probable transform	probable transform	hypothetical prote	coagulation factor	hypothetical prote	probable membrane	beta-glucosidase (carboxypeptidase D	probable two-compo	probable benzoate	ferredoxin-NADP re	embryogenesis prot	hypothetical prote	transcription fact	hypothetical prote	regulatory protein	
	ID	\$55480	AF2162	D87363	T51274	H97236	JQ0107	T00582	H82590	JE0259	T32122	T08477	C72466	G91021	F85865	E64996	A47004	G72706	T03109	A44768	S44191	T36766	S23477	T40339	T12683	T18649	JC5805	B84673	F31277	
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	Query Match Length DB	240	336	499	478	408	597	331	222	200	242	358	617	099	099	099	2319	294	302	830	516	388	461	469	478	884	718	745	816	
ф	Query Match	34.1	33.5	32.3	32.0	31.7	30.2	29.9	29.6	29.6	29.3	29.3	29.3	29.0	29.0	29.0	29.0	28.7	28.7	28.7	28.4	28.0	28.0	28.0	28.0	28.0	27.7		27.7	
	Score	56	55	53	52.5	52	49.5	49	48.5	48.5	48	48	48	47.5	47.5	4.7.5	47.5	47	47	47	46.5	46	46	46	46	46	45.5	45.5	45.5	
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hypothetical prote coagulation factor tyrosine kinase gr ABA-induced plasma anthranilate synth hypothetical prote priplasmic sugar segmentation prote hypothetical prote membrane transport amidase (EC 3.5 histidine ammonia-hypothetical prote transport thypothetical prote transport this protection in the protection of the protection of the protection in the protection in the protection of the protection	probable membrane
BA0505 BZHU 1048862 1048862 144524 AB3093 AB3093 B98193 AZ5066 151197 100158 H89758 126490	S67675
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1355 106 106 106 1082 322 322 346 4837 638 638 675	815
222222222222222 	27.4
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0 11 12 18 18 18 18 18 18 18 18 18 18 18 18 18	45

ALIGNMENTS

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A Status: preliminary
A; Molecule type: DNA
A; Status: preliminary
A; Molecule type: DNA
A; Status: Preliminary
A; Molecule type: DNA
A; Cross-references: EMBL: Z49811; NID: 9854599; PIDN: CAA89952.1; PID: 9854601
B; Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
Submitted to the EMBL Data Library, May 1995
A; Reference number: Z21821
A; Reference number: Z21821
A; Reference number: Z21821
A; Reference number: Z21821
A; References: Preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-240 cCCO2>
A; Residues: 1-240 cCCO2>
A; Residues: 1-240 cCCO2>
A; Residues: Latus BMBL: Z49811; PIDN: CAA89952.1; GSPDB: GN00066; SPDB: SPAC5H10.02c
A; Experimental source: strain 972h-; cosmid c5H10
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hypothetical protein SPAC5H10.02c - fission yeast (Schizosaccharomyces pombe)
                                        C;Species: Schizosaccharomyces pombe
C;Date: 01-Ang-1995 #sequence_revision 01-Sep-1995 #text_change 10-Dec-1999
C;Accession: S55480; 173866
R;Connor, R.; Churcher, C.M.
submitted to the EMBL Data Library, May 1995
A;Reference number: S55479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: SPDB:SPAC5H10.02c
A;Map position: 1
C;Superfamily: conserved hypothetical protein YMR322c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 57.9
Matches 11; Conservative
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11 AAACHGHLLLGNPKNSASV 29 δŏ

SAVCHGPVLLANVKNPQSV 156 138 qq

RESULT 2

AF2162

Upp-jucose 4-epimerase [imported] - Nostoc sp. (strain PCC 7120)

Upp-jucose 4-epimerase [imported] - Nostoc sp. (strain PCC 7120)

Upp-jucose s. Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002

C;Accession: AF2162

C;Accession: AF2162

C;Accession: AF2163

Nakazaki, N; Shimpo, S; Sugimoto, M; Takazawa, M; Yamada, M; Yasuda, M; Tabati DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; WUD:21595285; PMID:11759840

A;Accession: AF2162

A;Status: preliminary

A;Molecule type: DNA

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R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; K submitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome II BAC T27E13 genomic sequence.
A;Reference number: 214178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross references: EMDL: AC004165; NID: 93150396; PID: 93150404
A; Experimental source: cultivar Columbia
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
                                                DNA repair exonuclease [imported] - Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: 14-sep-2001 #sequence_revision 14-Sep-2001 #text_change 16-Aug-2002 C; Accession: H97236 R; Nolling, J.; Breton, G.; Cmelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L.; Dalty, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001 A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A; Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE001437; PIDN:AAK80683.1; PID:g15025773; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical 66K protein - Ononis yellow mosaic virus C;Species: Ononis yellow mosaic virus C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999 C;Date: 07-Sep-1990 Mtext_change 08-O
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Pred. No. 16;
5; Mismatches 6; Indels
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C;Superfamily: exonuclease sbcD; phosphoesterase core homology
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Pred. No. 53;
4; Mismatches 9;
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A; Molecule type: DNA
A; Residues: 1-331 <ROU>
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92 VAAGPLARDHGIIMVGTPKS 111
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Best Local Similarity 37.5%;
Matches 12; Conservative 4
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Best Local Similarity 45.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-408 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: H97236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conserved hypothetical protein CC0920 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Accession: D87363
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
R;Nierman, M.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
R;Nierman, M.C.; Feldblyum, T.V.; Paulsen, T.V.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: al12853
C;Superfamily: Bscherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology
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                          A;Cross-references: GB:BA000019; PIDN:BAB74552.1; PID:g17131947; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                   Length 336;
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Pred. No. 14;
1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Indels
                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: cultivar Columbia; BAC clone T8M16
                                                                                                                                                                                                                                                                                                                           13;
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                                                                                                                                                                                                                                                   DB 2;
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                                                                                                                                                                                                                                                Score 55; DB Pred. No. 5.2;
                                                                                                                                                                                                                                                                                                                                                                                              1 IKDSHLGAGPAAACHGHLLLGNPKNSASVSK 31
                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 DARAGEGFARHCHGDLHLGN 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 DSHLGAGPAAACHGHLLLGN 22
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1 Similarity 55.0%;
11; Conservative
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1 Similarity 45.5%;
10; Conservative
                                                                                                                                                                                                                                                ch 33.5%;
1 Similarity 35.5%;
11; Conservative
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Best Local Similarity
Matches 11; Conserva
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Best Local Similarity
Matches 11; Conserv
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-499 <STO>
A; Residues: 1-336 <KUR>
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A; Note: T8M16_190
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N; Contains: oxidoreductase (EC 1.-.-.)
C; Species: Orytchagus cuniculus (domestic rabbit)
C; Species: Orytchagus cuniculus (domestic rabbit)
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Mar-2000
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Mar-2000
C; Accession: JE00259
R; Yamamoto, Y; Ishizuka, M.; Takada, A.; Fujita, S.
J; Blochem. 124, 503-508, 1998
A; Title: Cloning, tissue distribution, and functional expression of two novel rabbit
A; Reference number: JE00258; WIID:98391821; PMID:9722658
A; Molecule type: MRNA
A; Residues: 1-500 «YAM>
A; Cross = references: DDBJ:AB0008785
C; Comment: This protein shows high drug metabolizing activity.
C; Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C; Repwords: chromoptorieln; electron transfer; endoplasmic reticulum; heme; iron; meti
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R; Thorsted, P.B.; Shah, D.S.; Macartney, D.; Kostelidou, K.; Thomas, C.M.
Plasmid 36, 95-111, 1996
A; Title: Conservation of the genetic switch between replication and transfer genes o
A; Reference number: 216434; MUID:97118926; PMID:8954881
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-242 < GRA>
A; Residues: 1-242 < GRA>
A; Cross references: EMBL:AF016685; PIDN: AAB66219.1; GSPDB:GN00023; CESP:F59E11.5
A; Experimental source: strain Bristol N2; clone F59E11
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C; Species: Caenorhabditis elegans
C; Species: 29-oct-1999 #sequence_revision 29-oct-1999 #text_change 29-oct-1999
C; Accession: T32122
R; Bradshaw, H.
Stradshaw, H.
Stradshaw, H.
Sherited to the EMBL Data Library, July 1997
A; Description: The sequence of C. elegans cosmid F59E11.
A; Reference number: 221124
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
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F;305-468/Domain: transmembrane #450 homology <CYP>
F;310-326/Domain: transmembrane #status predicted <TM2>
F;446/Binding site: heme iron (Cys) (axial ligand) #status predicted
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29.3%; Score 48; DB 2; Length 242;
Best Local Similarity 39.3%; Pred. No. 36;
Matches 11; Conservative 4; Mismatches 13; Indels
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A;Introns: 87/3; 123/3; 180/3; 217/3
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Best Local Similarity 55.6%;
Matches 10; Conservative
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A;Gene: CESP:F59E11.5
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C; Species: Xylella fastidiosa
C; Species: Xylella fastidiosa
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 01-Mar-2002
C; Accession: H82590
C; Accession: H82590
R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequent Nature 406, 151-157, 2000
A; Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A; Reference number: A82515; MUID:20365717; PMID:10910347
A; Note: for a complete list of authors see reference number A59328 below
A; Accession: H82590
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                M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, ieuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
                                                                                            A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID: 20083487; PMID: 10617197
A; Accession: C84705
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C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                             A; Cross-references: GB: AE002093; NID: 93150404; PIDN: AAC16956.1; GSPDB: GN00139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 331;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 LGAGPAAACH-----GHLLLGNPKNSAS 28
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Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49;
Pred. No.
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61.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 29.9
Best Local Similarity 45.2
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                           A; Gene: At2g30160; T27E13.10
                                                                                                                                                                                                                                                                                                                                                                                                                                     C, Keywords: mitochondrion
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                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-331 <STO>
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                                                                                                                                                                                                A;Status: preliminary
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Matches
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H82590
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A.Accession: T08477 A.Status: preliminary; translated from GB/EMBL/DDBJ A.Molecule type: DNA A.Residues: 1-358 <- THO>

170 HGHLWLLNQPPNPSSASK 187

g

cytochrome P450 2D24 - rabbit

RESULT 9

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hypothetical protein b2255 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: E64996
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: E64996
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DMA
A; Molecule type: DMA
A; Residues: 1-660 CBLAT>
A; Cross-references: GB:AE000315; GB:U00096; NID:91788582; PIDN:AAC75315.1; PID:917885
A; Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                              R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May iller, L.; Plunkett III, G.; Burland, V.; Dimalanta, E.; Potamousis, K.; Apoda iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli Ol57:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Accession: F85865
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-660 < GTO>
A; Cross-references: GB: AE005174; NID: G12516601; PIDN: AAG57386.1; GSPDB: GN00145; UWGP:
A; Experimental source: strain Ol57:H7, substrain EDI933
                                      probable transformylase 23513 [imported] - Escherichia coli (strain 0157:H7, substrai Cispeciaes: Escherichia coli (cibate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 Cisacession: F85865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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29.0%; Score 47.5; DB 2;
Best Local Similarity 42.1%; Pred. No. 1.1e+02;
Matches 8; Conservative 6; Mismatches 4;
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Pred. No. 1.1e+02;
6; Mismatches 4;
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Job time : 5.40244 secs
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558 CDGEIINIGNPENEASIEE 576
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558 CDGEIINIGNPENEASIEE 576
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Best Local Similarity 42.1%;
Matches 8; Conservative t
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C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: G91021
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gencha, Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; F
DNA Res. 6, 83-101, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: translation initiation factor IF-2; translation elongation factor Tu homd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable translation initiation factor aIF-2 APB2374 [similarity] - Aeropyrum pernix (st
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: C72466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy; A; Reference number: A72450; MUID:99310339; PMID:10382966 A; Accession: C72466
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
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A;Experimental source: strain Kl
A;Cross-references: EMBL:U67194; NID:g1572520; PIDN:AAC64421.1; PID:g1572526
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Pred. No. 1.1e+02;
6; Mismatches 4; Indels
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29.3%; Score 48; DB 2; Length 617;
Best Local Similarity 27.6%; Pred. No. 88;
Matches 8; Conservative 8; Mismatches 13; Indels
                                                                                                                                                                                    Query Match
29.3%; Score 48; DB 2; Length 358;
Best Local Similarity 58.8%; Pred. No. 52;
Matches 10; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :::: || | : | :|:| | : | :|:531 LEEARLGAAVAVSIQGRILIGRHANEGDI 559
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558 CDGEIINIGNPENEASIEE 576
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42.1%;
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Best Local Similarity 42.13
Matches 8; Conservative
                                                   C;Genetics:
A;Gene: incCl
A;Genome: plasmid R751
C;Superfamily: incC protein
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A; Molecule type: DNA
A; Residues: 1-660 <HAY>
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A;Molecule type: DNA
A;Residues: 1-617 <KAW>
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